

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 13, 2002, 10:15:56 ; Search time 14.7 seconds

(without alignments)  
1404.056 Million cell updates/sec

Title: US-09-695-293-42

Perfect score: 4422

Sequence: 1 METKGYHSLEPGIDMERRMG.....FLTFAPDLVFNELLARYREG 845

Scoring table: BIOSUM62

Gapop 10.0 , Gapect 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents, AA:\*

1: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep:\*

2: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep:\*

3: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep:\*

4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep:\*

5: /cgn2\_6/ptodata/2/1aa/6C.COMB.pep:\*

6: /cgn2\_6/ptodata/2/1aa/Backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4385	99.2	984	US-08-764-870-15	Sequence 15, Appl
2	4385	99.2	984	US-08-980-115-15	Sequence 15, Appl
3	856	19.4	777	US-08-764-870-13	Sequence 13, Appl
4	856	19.4	777	US-08-980-115-13	Sequence 13, Appl
5	845.5	19.1	795	US-07-716-827C-5	Sequence 5, Appl
6	801	18.1	933	US-08-764-870-14	Sequence 14, Appl
7	801	18.1	933	US-08-980-115-14	Sequence 14, Appl
8	732.5	16.6	5223606-6	Patent No. 5223606	Sequence 11, Appl
9	726	16.4	918	US-09-041-886-11	Sequence 11, Appl
10	713.5	16.1	356	5223606-7	Patent No. 5223606
11	686.5	15.5	452	US-08-764-870-16	Sequence 16, Appl
12	686.5	15.5	452	US-08-980-115-16	Sequence 16, Appl
13	445.5	10.1	595	US-08-764-870-12	Sequence 12, Appl
14	445.5	10.1	595	US-08-980-115-12	Sequence 12, Appl
15	442.5	10.0	591	US-08-836-620A-17	Sequence 17, Appl
16	442.5	10.0	595	US-09-041-886-35	Sequence 35, Appl
17	438	9.9	596	US-08-836-620A-16	Sequence 16, Appl
18	417	9.4	548	US-09-139-617-1	Sequence 1, Appl
19	410	9.3	418	US-09-141-000-6	Sequence 6, Appl
20	410	9.3	435	US-09-040-508-2	Sequence 2, Appl
21	410	9.3	435	US-09-500-654-2	Sequence 2, Appl
22	410	9.3	458	US-09-141-000-4	Sequence 4, Appl
23	406.5	9.2	484	US-08-836-620A-14	Sequence 14, Appl
24	406.5	9.2	485	US-08-836-620A-5	Sequence 5, Appl
25	405	9.2	384	US-08-836-620A-15	Sequence 15, Appl
26	404.5	9.1	485	US-08-836-620A-3	Sequence 3, Appl
27	403.5	9.1	484	US-08-836-620A-13	Sequence 13, Appl

28	403.5	9.1	485	US-08-836-620A-2	Sequence 2, Appl
29	401	9.1	410	5223606-5	Patent No. 5223606
30	387.5	8.8	518	US-08-836-620A-18	Sequence 18, Appl
31	381	8.6	89	US-08-087-151-3	Sequence 3, Appl
32	381	8.6	89	US-08-561-072-3	Sequence 3, Appl
33	374	8.5	431	US-08-836-620A-19	Sequence 19, Appl
34	373	8.4	500	US-09-141-000-2	Sequence 2, Appl
35	360	8.1	66	5217867-1	Patent No. 5217867
36	343.5	7.8	284	US-08-592-214A-24	Sequence 24, Appl
37	343.5	7.8	284	US-08-659-188-20	Sequence 20, Appl
38	343.5	7.8	284	US-08-655-227-20	Sequence 20, Appl
39	343.5	7.8	284	US-08-655-241-20	Sequence 20, Appl
40	343.5	7.8	284	US-09-149-976-24	Sequence 24, Appl
41	343.5	7.8	284	US-09-398-326-20	Sequence 20, Appl
42	325	7.3	534	US-08-875-223-8	Sequence 8, Appl
43	317.5	7.2	533	US-07-952-800-2	Sequence 2, Appl
44	315.5	7.1	467	US-08-336-408B-4	Sequence 4, Appl
45	315.5	7.1	467	PCT-US91-00399-4	Sequence 4, Appl

## ALIGNMENTS

RESULT 1  
US-08-764-870-15  
Sequence 15, Application US/08764870  
Patent No. 6236946  
GENERAL INFORMATION:  
APPLICANT: Scanlan, Thomas S  
APPLICANT: Baxter, John D  
APPLICANT: Fletcherick, Robert J  
APPLICANT: Wagner, Richard L  
APPLICANT: Kushner, Peter J  
APPLICANT: Apriletti, James W  
APPLICANT: West, Brian  
TITLE OF INVENTION: Nuclear Receptor Ligands and Ligand  
NUMBER OF INVENTIONS: 16  
TITLE OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooley Godward  
STREET: Five Palo Alto Square, 3000 El Camino Real  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/764,870  
FILING DATE: 13-DEC-1996  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/008,540  
FILING DATE: 13-DEC-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/008,543  
FILING DATE: 13-DEC-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/008,606  
FILING DATE: 14-DEC-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Nakamura, Jackie N  
REGISTRATION NUMBER: 35,966  
REFERENCE/DOCKET NUMBER: UCAL-246/01US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650)843-5000  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 984 amino acids  
TYPE: amino acid

STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-764-870-15

```

Query Match          99.2%; Score 4385; DB 4; Length 984;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 837; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 METKGYSLPGGLDMERRMGVSOAVERSSLGPTERTDENNYMEIVAVSCGAIPNNST 60
Db 1 METKGYSLPGGLDMERRMGVSOAVERSSLGPTERTDENNYMEIVAVSCGAIPNNST 60
OY 61 QGSSKEKELLPCLOQDNNRPGILTSIDIKTELESKEISATVAESMGLYMSVRADYSYE 120
Db 61 QGSSKEKELLPCLOQDNNRPGILTSIDIKTELESKEISATVAESMGLYMSVRADYSYE 120
OY 121 QONOGSMSPAKIYONVQLYKFYKNGHRPSTLSCVNTPLRSPMSDSSGVNGVMRAI 180
Db 121 QONOGSMSPAKIYONVQLYKFYKNGHRPSTLSCVNTPLRSPMSDSSGVNGVMRAI 180
OY 181 VSPIMCHEKSPSVCSPLNMTSSVCSFAGINSSTTASFSGSPVHSPITTOGTLTCSPN 240
Db 181 VSPIMCHEKSPSVCSPLNMTSSVCSFAGINSSTTASFSGSPVHSPITTOGTLTCSPN 240
OY 241 AENRGSRSHPAHASNVGSPPLSSMKSSTSSPPSHCSYKSPVSPNNVTLRSSVSP 300
Db 241 AENRGSRSHPAHASNVGSPPLSSMKSSTSSPPSHCSYKSPVSPNNVTLRSSVSP 300
OY 301 ANINNSRCSVSSPMTNNRSTLSSPAASTVGSICSPVNNAFSTASGTSAGSSTLRDVP 360
Db 301 ANINNSRCSVSSPMTNNRSTLSSPAASTVGSICSPVNNAFSTASGTSAGSSTLRDVP 360
OY 361 SPDTQEKGAQEVPPFKTEVEESAIISNGYTGQNTIYQYIKPEPDGAFSSCLGNSKINS 420
Db 361 SPDTQEKGAQEVPPFKTEVEESAIISNGYTGQNTIYQYIKPEPDGAFSSCLGNSKINS 420
OY 421 SSESVPYIKQESTKHSCTGSEFKGNPTVNPFPMDGSYFSFMDKDYIYLSGLIGPPVPGF 480
Db 421 SSESVPYIKQESTKHSCTGSEFKGNPTVNPFPMDGSYFSFMDKDYIYLSGLIGPPVPGF 480
OY 481 DGNCGSGFPVGIKQEPDGGSYTPEASIPSSALIVGNSSGGSFHRIGAQCTISLSRSAR 540
Db 481 DGNCGSGFPVGIKQEPDGGSYTPEASIPSSALIVGNSSGGSFHRIGAQCTISLSRSAR 540
OY 541 DOSFOHLSFPVNTLVESMKS HGDLSRRSDGYPVLEYIPENVSSSTLRSSVSTGSSRPS 600
Db 541 DOSFOHLSFPVNTLVESMKS HGDLSRRSDGYPVLEYIPENVSSSTLRSSVSTGSSRPS 600
OY 601 KICLVCGDEASGCHYGVTCGSKYEFKRAVHGQNHVYLCAGNDCITIDKIRKNCPCACRL 660
Db 601 KICLVCGDEASGCHYGVTCGSKYEFKRAVHGQNHVYLCAGNDCITIDKIRKNCPCACRL 660
OY 661 QKCLQAGMNLGAKSKKLGKIGIHEOPQOQOOPPPPPPOSPEHGTYIAPAKEPSVN 720
Db 661 QKCLQAGMNLGAKSKKLGKIGIHEOPQOQOOPPPPPPOSPEHGTYIAPAKEPSVN 720
OY 721 TALVPOLSTISRALTSPVAVLENIEPEIYAGYDSSKPDIAENLSTNRLAGKOMIOY 780
Db 721 TALVPOLSTISRALTSPVAVLENIEPEIYAGYDSSKPDIAENLSTNRLAGKOMIOY 780
OY 781 VKAKAVLPGKKNLPLEDQITLLOYSMKCLSSPALSRSKTKHNSQOLYRAPDLVENE 837
Db 781 VKAKAVLPGKKNLPLEDQITLLOYSMKCLSSPALSRSKTKHNSQOLYRAPDLVENE 837

```

RESULT 2  
US-08-980-115-15  
; Sequence 15, Application US/09980115  
; Patent No. 626622  
; GENERAL INFORMATION:  
; APPLICANT: Scanlan, Thomas S.

```

; APPLICANT: Baxter, John D.
; APPLICANT: Fletterick, Robert J.
; APPLICANT: Wagner, Richard L.
; APPLICANT: Kushner, Peter J.
; APPLICANT: Apriletti, James W.
; APPLICANT: West, Brian L.
; APPLICANT: Shiau, Andrew K.
; TITLE OF INVENTION: NUCLEAR RECEPTOR LIGANDS AND LIGAND BINDING DOMAINS
; FILE REFERENCE: UCAL-246/02US
; CURRENT APPLICATION NUMBER: US/08/980,115
; EARLIER FILING DATE: 1997-11-26
; EARLIER APPLICATION NUMBER: 08/764,870
; EARLIER FILING DATE: 1996-12-13
; EARLIER APPLICATION NUMBER: 60/008,606
; EARLIER FILING DATE: 1995-12-14
; EARLIER APPLICATION NUMBER: 60/008,543
; EARLIER FILING DATE: 1995-12-13
; EARLIER APPLICATION NUMBER: 60/008,540
; NUMBER OF SEQ. ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 984
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (695)..(969)
; OTHER INFORMATION: minimal ligand binding domain
US-08-980-115-15

Query Match          99.2%; Score 4385; DB 4; Length 984;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 837; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 METKGYSLPGGLDMERRMGVSOAVERSSLGPTERTDENNYMEIVAVSCGAIPNNST 60
Db 1 METKGYSLPGGLDMERRMGVSOAVERSSLGPTERTDENNYMEIVAVSCGAIPNNST 60
OY 61 QGSSKEKELLPCLOQDNNRPGILTSIDIKTELESKEISATVAESMGLYMSVRADYSYE 120
Db 61 QGSSKEKELLPCLOQDNNRPGILTSIDIKTELESKEISATVAESMGLYMSVRADYSYE 120
OY 121 QONOGSMSPAKIYONVQLYKFYKNGHRPSTLSCVNTPLRSPMSDSSGVNGVMRAI 180
Db 121 QONOGSMSPAKIYONVQLYKFYKNGHRPSTLSCVNTPLRSPMSDSSGVNGVMRAI 180
OY 181 VSPIMCHEKSPSVCSPLNMTSSVCSFAGINSSTTASFSGSPVHSPITTOGTLTCSPN 240
Db 181 VSPIMCHEKSPSVCSPLNMTSSVCSFAGINSSTTASFSGSPVHSPITTOGTLTCSPN 240
OY 241 AENRGSRSHPAHASNVGSPPLSSMKSSTSSPPSHCSYKSPVSPNNVTLRSSVSP 300
Db 241 AENRGSRSHPAHASNVGSPPLSSMKSSTSSPPSHCSYKSPVSPNNVTLRSSVSP 300
OY 301 ANINNSRCSVSSPMTNNRSTLSSPAASTVGSICSPVNNAFSTASGTSAGSSTLRDVP 360
Db 301 ANINNSRCSVSSPMTNNRSTLSSPAASTVGSICSPVNNAFSTASGTSAGSSTLRDVP 360
OY 361 SPDTQEKGAQEVPPFKTEVEESAIISNGYTGQNTIYQYIKPEPDGAFSSCLGNSKINS 420
Db 361 SPDTQEKGAQEVPPFKTEVEESAIISNGYTGQNTIYQYIKPEPDGAFSSCLGNSKINS 420
OY 421 SSESVPYIKQESTKHSCTGSEFKGNPTVNPFPMDGSYFSFMDKDYIYLSGLIGPPVPGF 480
Db 421 SSESVPYIKQESTKHSCTGSEFKGNPTVNPFPMDGSYFSFMDKDYIYLSGLIGPPVPGF 480
OY 481 DGNCGSGFPVGIKQEPDGGSYTPEASIPSSALIVGNSSGGSFHRIGAQCTISLSRSAR 540
Db 481 DGNCGSGFPVGIKQEPDGGSYTPEASIPSSALIVGNSSGGSFHRIGAQCTISLSRSAR 540
OY 541 DOSFOHLSFPVNTLVESMKS HGDLSRRSDGYPVLEYIPENVSSSTLRSSVSTGSSRPS 600

```

Db 541 DQSFQHLSSPPVNTLVESKSHGDLSSRSDDGTPVLEIIPENWSSSTLSSVSTGSSRPS 600  
QY 601 KICLVGDEASGCHGVVTCGSGKVFPEKRAVEGQHNLYLCAGRNDCCIIDKIRKNCPCARL 660  
Db 601 KICLVGDEASGCHGVVTCGSGKVFPEKRAVEGQHNLYLCAGRNDCCIIDKIRKNCPCARL 660  
QY 661 QKCLQGMNIGARKSKKLGKLGHEHQPOQOQPPPPPPPPSEETTYIAPAKESVN 720  
Db 661 QKCLQGMNIGARKSKKLGKLGHEHQPOQOQPPPPPPPPSEETTYIAPAKESVN 720  
QY 721 TALVPOLSTSRALTPSPVAVLENIPEEIVYAGYDSSKPTAEULSTLNRKLGKQMIQY 780  
Db 721 TALVPOLSTSRALTPSPVAVLENIPEEIVYAGYDSSKPTAEULSTLNRKLGKQMIQY 780  
QY 781 VKMAKVLPGFKNLPLEDOITLIQYSWMCJSSFALSWSRYKHTNSQFLYFAPDLVFN 837  
Db 781 VKMAKVLPGFKNLPLEDOITLIQYSWMCJSSFALSWSRYKHTNSQFLYFAPDLVFN 837

RESULT 3  
US-08-764-870-13  
; Sequence 13, Application US/08764870  
; Patent No. 6236946  
; GENERAL INFORMATION:  
; APPLICANT: Scanlan, Thomas S  
; APPLICANT: Baxter, John D  
; APPLICANT: Fletterick, Robert J  
; APPLICANT: Wagner, Richard L  
; APPLICANT: Kushner, Peter J  
; APPLICANT: Apriletti, James W  
; TITLE OF INVENTION: Nuclear Receptor Ligands and Ligand  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooley Godward  
; STREET: Five Palo Alto Square, 3000 El Camino Real  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94306  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/764,870  
; FILING DATE: 13-DEC-1996  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/008,540  
; FILING DATE: 13-DEC-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/008,543  
; FILING DATE: 13-DEC-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/008,606  
; FILING DATE: 14-DEC-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Nakamura, Jackie N  
; REGISTRATION NUMBER: 35,966  
; REFERENCE/DOCKET NUMBER: UCAL-246/0105  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650)843-5000  
; INFORMATION FOR SEQ. ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 777 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

US-08-764-870-13  
Query Match 19.4%; Score 856; DB 4; Length 777;  
Best Local Similarity 35.0%; Pred. No. 3e-55;  
Matches 239; Conservative 83; Mismatches 212; Indels 148; Gaps 25;

QY 248 SHSFAHASNNGSPPLSSPLSSKSSISPPSHCSKYSKVSPPNNVTLRSSVSPANNINRS 307  
Db 6 SLTPGRENPSSVLAQERGDVMDFYKLRGATVKVASSPS-----LAVASQSDSKORR 60  
QY 308 CSVSPSPNTNRS---TLSSPASTVG---SICSPVNNAFSTYASG---TSAGSSTLR 356  
Db 61 LLDVFPKGSVNAQOPLDSRAVSLSMGLYMGFTTKWGNLDLGFPOQOISLSSGETDLK 120  
QY 357 DVVPS-----PPTQKGAQ-----EVPFKTEVEESAISNGVTGLNIYOYI 398  
Db 121 LLESIANLNRSSTVPENPSSASTAVSAAPTEKEPKTHSDVSSBQHLKQ----- 173  
QY 399 KPEPDGAFSSSCILGKNSKI--NSDSSFV-----PKQESTYHSCSGTFFKGNPT 446  
Db 174 -----TGTNGVKNKLYTTDQSTFDLQDLFFSSGSPKETNESPMWRSDLLIDENCL 224  
QY 447 VNPPFMDGSYF-----SEMDKDY--SLSGILGPPVPGDNC 485  
Db 225 LSLPAGEDDSFLLEGNSNEDCKPLLPDTPKIKDNGDLVSSPNTLPOV-----KTE 279  
QY 486 GSGF-----PYGIKQEPDDGSYPEASIPSSAIVG-----VNSGQSFHYRIGA 529  
Db 280 KEDFIELCTGVIKQF-KLGIVYQASFPGANIIGNKMSAISVHGVSFGGOMYHDM-- 336  
QY 530 QGTISLSRSARDOFQHLSSPPVNTLVESW---KSHGD--LSRSRDGYVLEYIBNV 584  
Db 337 -NTASLSQO--QDOK-PIFNVTPIPIVGSSEMNRCQGGSDNLTSLGLTNPFGRTVFSNGY 393  
QY 585 SSSTLR-----SVSTGSS-RPSKICLVGDEASGCHGVVTCGSKVFEKRAVEGQ 635  
Db 394 SSPSMRPDVSSPSSSSSTATTGPPKLCVCSDAASGCHGVLCGCKVFEKRAVEGQ 453  
QY 636 NYLCAGRNDCCIIDKIRKNCPCARLQKLCQAGMNLGARKSKKLGKLGHEHQPOQOOP 695  
Db 454 NYLCAGRNDCCIIDKIRKNCPCARLQKLCQAGMNLGARKSKKLGKLGHEHQPOQOOP 695  
QY 696 PPPPPQSPERGTYIAPAKESVNTALVOLSTISALTPSPVAVLENIPEEIVYAGYD 755  
Db 505 TGVQSETSSENGKNTIVPATLPQ-----LPTLVSLLEVEIEPELVYAGYD 549  
QY 756 SKRPDTEENLSTLNRKLGKQMIQVVKMAKVLPGFKNLPLEDOITLIQYSWMCJSSFALS 815  
Db 550 SSVPDSTWRIWTTILNMGKROVIAVVKAKAIPGFRNLHDDQMTLQYSMFLMAFRLG 609  
QY 816 WRSYKHTNSQFLYFAPDLVFN 837  
Db 610 WRSYKHTNSQFLYFAPDLVFN 837

RESULT 4  
US-08-980-115-13  
; Sequence 13, Application US/08980115  
; Patent No. 626622  
; GENERAL INFORMATION:  
; APPLICANT: Scanlan, Thomas S.  
; APPLICANT: Baxter, John D.  
; APPLICANT: Fletterick, Robert J.  
; APPLICANT: Wagner, Richard L.  
; APPLICANT: Kushner, Peter J.  
; APPLICANT: Apriletti, James W.  
; APPLICANT: Shiau, Andrew K.  
; TITLE OF INVENTION: NUCLEAR RECEPTOR LIGANDS AND LIGAND BINDING DOMAINS  
; FILE REFERENCE: UCAL-246/0205  
; CURRENT APPLICATION NUMBER: US/08/980,115  
; CURRENT FILING DATE: 1997-11-26







Db 673 FTF-----SPGDDIOLIPPL-----INLMSIEPDVIVAGHONTKPDTSLSLT 716  
QY 768 TTNRLAGKMIQVYKAKVLPFGKNLPLEDQITLLIQYSWMLCSFALSWRSYKHTNSOFL 827  
Db 717 SLNOLGEROLLSVYKSKSLPGFRNLHIDQITLLIQYSWMLSMVFGOLGRSYKHTNSOGL 776  
QY 828 YEAPDLVFNELLARRE 844  
Db 777 YEAPDLILNE--QRMKE 791

RESULT 7  
US-08-980-115-14  
; Sequence 14, Application US/08980115  
; Patent No. 6266622  
; GENERAL INFORMATION:  
; APPLICANT: Scanlan, Thomas S.  
; APPLICANT: Baxter, John D.  
; APPLICANT: Fletterick, Robert J.  
; APPLICANT: Wagner, Richard L.  
; APPLICANT: Kushner, Peter J.  
; APPLICANT: Arlietti, James W.  
; APPLICANT: West, Brian L.  
; APPLICANT: Shiau, Andrew K.  
; TITLE OF INVENTION: NUCLEAR RECEPTOR LIGANDS AND LIGAND BINDING DOMAINS  
; FILE REFERENCE: UCAL-246/0205  
; CURRENT APPLICATION NUMBER: US/08/980,115  
; EARLIER FILING DATE: 1997-11-26  
; EARLIER APPLICATION NUMBER: 08/764,870  
; EARLIER FILING DATE: 1996-12-13  
; EARLIER APPLICATION NUMBER: 60/008,606  
; EARLIER FILING DATE: 1995-12-14  
; EARLIER APPLICATION NUMBER: 60/008,543  
; EARLIER FILING DATE: 1995-12-13  
; EARLIER APPLICATION NUMBER: 60/008,540  
; EARLIER FILING DATE: 1995-12-13  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 14  
; LENGTH: 933  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: DOMAIN  
; LOCATION: (659)..(918)  
; OTHER INFORMATION: minimal ligand binding domain  
US-08-980-115-14

Query Match 18.1%; Score 801; DB 4; Length 933;  
Best Local Similarity 29.5%; Pred. No. 4, 8e-51;  
Matches 253; Conservative 95; Mismatches 221; Indels 288; Gaps 37;

QY 191 SPYVCSPLNMTSVSCSPAG-----INSVSTTASFGSPVHSPITQGT--PLTLC---SPNA 241  
Db 20 SPEVGSPL-----LCRPAAGPFPGSQTSPTLPEVSAIPIS---LDGILFFRPGCGODPSD 71  
QY 242 EN-----RGRKSHPAHASNVCSPPLSP-----LSSMKSSISSPPSHCVSKSPV 285  
Db 72 EKTODQOGLSDVEGAYSAEATRGAGSSSSPPEKDSGLDSVLDITLAP-----121  
QY 286 SSPNNVTLRSSVSSPANINNSRCSVSS-----PSNTNMRSTLSSPAATVGSICSP 336  
Db 122 SGPG-----QSQSPRPA-----CEVTSSWCLFGPELPED-----PPAAPATQRYLSP 163  
QY 337 VNNAFSYTAGSTAGSSTLRDVP---SPDTQ-----EKGAEVFPF-----KTE 378  
Db 164 LMSR--SGCKVGDSSGTAHAHVLPRLGSLPARQLLLPASESPHWSGAPVKPSPQAAYEVE 222  
QY 379 EYESAISNGVGOINIVQYIKPEP-----DGAFFSSSC-----LGKNSKI--NSDSSFSV 425  
Db 223 EEDSSESESGAPL-----LKGKPRALGAAAGGAACPPGAAAGVAVLPKEDSRSA 277

QY 426 P-----IKQES-----TKHSCSGTSFKG-----443  
Db 278 PRVALVEDAPMAPGRSPLATTWDFIHVPITLLPHALLAARTQOLLEDESDDGAGAAAS 337  
QY 444 -----NFTVNPFP-----FMDGSYFSPMDKD-----465  
Db 338 AFAPRTSPCASSTPVAVAGDPDCAVPPDAEPKDDAVPLYSDFQPPALKIKEEGEAAS 397  
QY 466 -----YYSLSGT-----LGPVP-----GFD 481  
Db 398 ARSPRSYLVAGANPAAPDFPLGPPPLPAPRATPSRPGEAANVTAPASVSSASSSGST 457  
QY 482 GNC-----EGSGPVGIKQEPDDGSYYPASISPAIVGNSSGOSFHY-RIGA 529  
Db 458 IHCILYKAGAPPOOGFPAPPPCKAPGASGCLLPDGLPSTISASAAAGAPALYPALGL 517  
QY 530 OCTISLSRSARDQSFQHLSSFPVNTLVESMKSHODLSRRSDGYPLEYI--PENVSST 588  
Db 518 NGLPOLGYQAAVILK-----EGLPQVVP-----PYLNYLRPSEASQS 554  
QY 589 LRSVSTGSSRPCKITLVCGEDEASGCHGYVTCGSKVFFKRAVEGQHNVLCAGNDICTD 648  
Db 555 PQ--VSFESLPQKICITLVCGEDEASGCHGYVTCGSKVFFKRAVEGQHNVLCAGNDICTD 612  
QY 649 KTRKNCPCARLOKCLQAGMNLGARKSKKLGKLGHE--EDPQQQPPPPPPPPQSPPEG 707  
Db 613 KTRKNCPCARLRCCKQAGMVLGGRKKFKNKVRVRLDAVALPQLGVPRESQALSOR 672  
QY 708 TYIAPAKESPVNTALPOLSTISRALTPSPVWLENTEPELVAGYSSKPDTEMLLS 767  
Db 673 FTF-----SPGDDIOLIPPL-----INLMSIEPDVIVAGHONTKPDTSLSLT 716  
QY 768 TTNRLAGKMIQVYKAKVLPFGKNLPLEDQITLLIQYSWMLCSFALSWRSYKHTNSOFL 827  
Db 717 SLNOLGEROLLSVYKSKSLPGFRNLHIDQITLLIQYSWMLSMVFGOLGRSYKHTNSOGL 776  
QY 828 YEAPDLVFNELLARRE 844  
Db 777 YEAPDLILNE--QRMKE 791

RESULT 8  
5223606-6  
; Patent No. 5223606  
; APPLICANT: BLAUDIN DE THE, HUGHES, MARCHIO, AGNES, TIOLLAIS,  
; PIERRE-DEJEAN, ANNE  
; TITLE OF INVENTION: STEROID/THYROID HORMONE RECEPTOR-RELATED  
; PROTEIN INAPPROPRIATELY EXPRESSED IN HUMAN HEPATOCELLULAR CARCINOMA  
; NUMBER OF SEQUENCES: 11  
; CURRENT APPLICATION DATA:  
; FILING DATE: 17-DEC-1987  
; PRIOR APPLICATION DATA:  
; SEQ ID NO: 6  
; LENGTH: 363  
5223606-6

Query Match 16.6%; Score 732.5; DB 6; Length 363;  
Best Local Similarity 57.0%; Pred. No. 1, 4e-46;  
Matches 138; Conservative 37; Mismatches 46; Indels 21; Gaps 5;

QY 603 CLVCGDEASGCHGYVTCGSKVFFKRAVEGQHNVLCAGNDICTIKTRKNCPCARLOK 662  
Db 1 CLICGDEASGCHGYVTCGSKVFFKRAVEGQHNVLCAGNDICTIKTRKNCPCARLOK 60  
QY 663 CLQAGMNLGARKSKKLGKLGHEEDPQQQPPPPPPPPQSPPEGTYIAPAKESPVNTA 722  
Db 61 CCGAGMVLGGRKKFKNKVR--VMRALDAVALPAPVGIPIES--ORITF-----SPQEOIO 112  
QY 723 LVPLSTISRALTPSPVWLENTEPELVAGYSSKPDTEMLLSLTNRLAGKMIQVYK 782  
Db 113 LIPL-----INLMSIEPDVIVAGHONTKPDTSLSLTSLNOLGEROLLSVYK 161

```

OY 763 WAKVLPGRKNLPLEJOIILLIOYSWMCCLASSFALSMYSKXHTNSOPLYFADPLFENELARY 842
Db 162 WSKSPGFRNLHIDQIULIOTSMWSLAVFGLGMSRYKHSVSCOMLPFADPLILNE--QRM 219
OY 843 RE 844
Db 220 KE 221

RESULT 9
US-09-041-886-11
: Sequence 11, Application US/09041886
: Patent No. 6235872
: GENERAL INFORMATION:
: APPLICANT: Bredesen, Dale E.
: APPLICANT: Rabizadeh, Sharroz
: TITLE OF INVENTION: Proapoptotic Peptides, Dependence
: TITLE OF INVENTION: Polypeptides and Methods of Use
: NUMBER OF SEQUENCES: 72
: CORRESPONDENCE ADDRESS:
: ADDRESS: Campbell & Flores LLP
: STREET: 4370 La Jolla Village Drive, Suite 700
: CITY: San Diego
: STATE: California
: COUNTRY: United States
: ZIP: 92122
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/041,886
: FILING DATE:
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Campbell, Cathryn A.
: REGISTRATION NUMBER: 31,815
: REFERENCE/DOCKET NUMBER: P-LJ 2626
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (619) 535-9001
: TELEFAX: (619) 535-8949
: INFORMATION FOR SEQ ID NO: 11:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 918 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-09-041-886-11

Query Match 16.4%, Score 726, DB 4, Length 918;
Best Local Similarity 29.5%, Pred. No. 1.7e-45;
Matches 229; Conservative 79; Mismatches 197; Indels 272; Gaps 31.

OY 228 SPNANRGRSRSSPMAHSAVSGSPSLSSPMKSSSISSPSSHCSYKSPVSPNNVTLRSSV 297
Db 90 SFOARRRGPTGYL-----VLDEEOP--SQPSALECHERCVCVPP-----GAAVAAASK 137
OY 298 SSPANINNSRCSVSSPSNTNNRSTLSPAASTVGSICSPVNNAFSTYASGTSAGSSTLRD 357
Db 138 GLPQGL-----PAPBEDD-----SAAPSTL-SLIGP-----TTFGLSSCSADLKD 177
OY 358 VYPSPDTOEKGAQEVPPFKRTEVESEAIISNGYTGQNLIVQYIKPEPDGAFSSS--CLGQN 414
Db 178 ILSEASTQOLLQOQ-----QOEAVSBSGSSSGRA-----REASGAPTSSKDNVLTGT 223
OY 415 SKINDS-----SFSYPIKQESTKHKSCGTSFKGN-----PTVNFPP----- 451
Db 224 STISDMAHELCAVSAVSKMGLVEALEHLSFPGQLKDCMYAPLGLVPAVRPTPCAPLAE 283
OY 452 ---FMDGSYSEFMDKDYVSLISGLGPPVPGFDG---NCEGS----- 487

```

[illegible]

RESULT 11  
US-08-764-870-16  
Sequence 16, Application US/08764870  
Patent No. 6236946  
GENERAL INFORMATION:  
APPLICANT: Scanlan, Thomas S  
APPLICANT: Baxter, John D  
APPLICANT: Pletterick, Robert J  
APPLICANT: Wagner, Richard L  
APPLICANT: Kushner, Peter J  
APPLICANT: Applelli, James W  
TITLE OF INVENTION: Nuclear Receptor Ligands and Ligand  
TITLE OF INVENTION: Binding Domains  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooley Goddard  
STREET: Five Palo Alto Square, 3000 El Camino Real  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/764,870  
FILING DATE: 13-DEC-1996  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/008,540  
FILING DATE: 13-DEC-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/008,543  
FILING DATE: 13-DEC-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/008,606  
FILING DATE: 14-DEC-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Nakamura, Jackie N  
REGISTRATION NUMBER: 35,966  
REFERENCE/DOCKET NUMBER: UCAL-246/01US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650)843-5000  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 452 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-764-870-16

Query Match 15.5%; Score 686.5; DB 4; Length 452;  
Best Local Similarity 48.2%; Pred. No. 5.2e-43;  
Matches 145; Conservative 33; Mismatches 66; Indels 57; Gaps 8;

QY 552 PNTLVES---WKS-----HGD--LSSRSDDGYPVLEYIPENVSSSTLRSVSTGSSRPS 600  
DB 47 PSPCTVKSEMGPMWMDSYSGPYGDMRLFTARDHVLPIIDYFP-----PQ 89  
QY 601 KICLVCGDEASGCHYGVVTCGSCVKFFKRAVEGQHNYICAGRNDCTIDKIRKNCPCARL 660  
DB 90 KTCILGCGKASGCHYGALTGSCVKFFKRAEGKQKYLCA SRNDCITDKFRKNCPCARL 149  
QY 661 OKCLDAGNLLARKSKKIKGLKGIHEBPPQOQOPPPPPPPQSPBEGTTIAPAKPEPVN 720  
DB 150 KRCYEAGMTLGARKLKLGNLK-LQEEGEASS-----TTSPTERT----- 189

QY 721 TALVPOLSTISR-----ALTPSPVWYLENIEPEIYAGYDSSKPDFAENLSTLNRLAGKQ 776  
DB 190 -----OKLTVSHIEGVECPFLFNVLAEIEGVCAGHDNQPDSFALLSLNLEGRQ 244  
QY 777 MIOVYKMAKVLPGFKNLPLEDQITLTOYSWMCLSSFALSWRSYKHTNSQFLYFAPDLVFN 836  
DB 245 LVHVYKMAKALPGFKNLHVDQMAVIOYSWMGLMVFANGMRSFTVNSRMLYFAPDLVFN 304  
QY 837 E 837  
DB 305 E 305

RESULT 12  
US-08-980-115-16  
Sequence 16, Application US/08980115  
Patent No. 6266622  
GENERAL INFORMATION:  
APPLICANT: Scanlan, Thomas S.  
APPLICANT: Baxter, John D.  
APPLICANT: Pletterick, Robert J.  
APPLICANT: Wagner, Richard L.  
APPLICANT: Kushner, Peter J.  
APPLICANT: Applelli, James W.  
APPLICANT: Shiau, Andrew K.  
TITLE OF INVENTION: NUCLEAR RECEPTOR LIGANDS AND LIGAND BINDING DOMAINS  
FILE REFERENCE: UCAL-246/02US  
CURRENT APPLICATION NUMBER: US/08/980,115  
EARLIER FILING DATE: 1997-11-26  
EARLIER APPLICATION NUMBER: 08/764,870  
EARLIER FILING DATE: 1996-12-13  
EARLIER APPLICATION NUMBER: 60/008,606  
EARLIER FILING DATE: 1995-12-14  
EARLIER APPLICATION NUMBER: 60/008,543  
EARLIER FILING DATE: 1995-12-13  
EARLIER APPLICATION NUMBER: 60/008,540  
EARLIER FILING DATE: 1995-12-13  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 16  
LENGTH: 452  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: DOMAIN  
LOCATION: (184)...(437)  
OTHER INFORMATION: minimal ligand binding domain  
US-08-980-115-16

Query Match 15.5%; Score 686.5; DB 4; Length 452;  
Best Local Similarity 48.2%; Pred. No. 5.2e-43;  
Matches 145; Conservative 33; Mismatches 66; Indels 57; Gaps 8;

QY 552 PNTLVES---WKS-----HGD--LSSRSDDGYPVLEYIPENVSSSTLRSVSTGSSRPS 600  
DB 47 PSPCTVKSEMGPMWMDSYSGPYGDMRLFTARDHVLPIIDYFP-----PQ 89  
QY 601 KICLVCGDEASGCHYGVVTCGSCVKFFKRAVEGQHNYICAGRNDCTIDKIRKNCPCARL 660  
DB 90 KTCILGCGKASGCHYGALTGSCVKFFKRAEGKQKYLCA SRNDCITDKFRKNCPCARL 149  
QY 661 OKCLDAGNLLARKSKKIKGLKGIHEBPPQOQOPPPPPPPQSPBEGTTIAPAKPEPVN 720  
DB 150 KRCYEAGMTLGARKLKLGNLK-LQEEGEASS-----TTSPTERT----- 189  
QY 721 TALVPOLSTISR-----ALTPSPVWYLENIEPEIYAGYDSSKPDFAENLSTLNRLAGKQ 776  
DB 190 -----OKLTVSHIEGVECPFLFNVLAEIEGVCAGHDNQPDSFALLSLNLEGRQ 244  
QY 777 MIOVYKMAKVLPGFKNLPLEDQITLTOYSWMCLSSFALSWRSYKHTNSQFLYFAPDLVFN 836  
DB 245 LVHVYKMAKALPGFKNLHVDQMAVIOYSWMGLMVFANGMRSFTVNSRMLYFAPDLVFN 304





This Page Blank (uspto)

---

**This Page Blank (usp10)**



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

# OM protein - protein search, using sw model

Run on: September 13, 2002, 10:15:56 ; Search time 36.28 Seconds  
(without alignments)  
2587.027 Million cell updates/sec

Title: US-09-695-293-42

4422

Perfect score: 1 METKGYHSLPGLMERKRG.....FLYFAPDLVFENLLARVREG 845

Sequence:

## Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database :

A\_Geneseq.032802.\*  
1: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1980.DAT.\*  
2: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1981.DAT.\*  
3: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1982.DAT.\*  
4: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1983.DAT.\*  
5: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1984.DAT.\*  
6: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1985.DAT.\*  
7: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1986.DAT.\*  
8: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1987.DAT.\*  
9: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1988.DAT.\*  
10: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1989.DAT.\*  
11: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1990.DAT.\*  
12: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1991.DAT.\*  
13: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1992.DAT.\*  
14: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1993.DAT.\*  
15: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1994.DAT.\*  
16: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1995.DAT.\*  
17: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1996.DAT.\*  
18: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1997.DAT.\*  
19: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1998.DAT.\*  
20: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1999.DAT.\*  
21: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA2000.DAT.\*  
22: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4385	99.2	984	20	AAV21622
2	4377	99.0	984	9	AAAP80927
3	856	19.4	777	9	AAAP80919
4	856	19.4	777	18	AAWA4700
5	856	19.4	777	20	AAV21623
6	845.5	19.1	1070	18	AAW17789
7	806	18.2	933	21	AAI97297
8	801	18.1	933	20	AAV21621
9	758.5	17.2	902	10	AAAP93110
10	758.5	17.2	902	10	AAAP91006
11	753.5	17.0	902	12	AAW12224

12	731.5	16.5	919	18	AAW14783	Androgen receptor.
13	731.5	16.5	919	21	AAV78914	Human androgen rec
14	726	16.4	918	20	AAV33491	Human androgen rec
15	725.5	16.4	919	10	AAAP93109	Human androgen rec
16	723	16.4	918	12	AAW12223	Human androgen rec
17	723	16.4	919	10	AAAP90996	Human androgen rec
18	686.5	15.5	452	20	AAV21627	Ligand binding dom
19	666.5	15.1	630	12	AAW12230	TRP/androgen rece
20	445.5	10.1	595	20	AAV21626	Ligand binding dom
21	445.5	10.1	595	22	AAAG84505	Human oestrogen re
22	445.5	10.1	595	22	AAAG84506	Human oestrogen re
23	445.5	10.1	595	22	AAAG84507	Human oestrogen re
24	445.5	10.1	595	22	AAAG84509	Human oestrogen re
25	445.5	10.1	595	22	AAAG84510	Human oestrogen re
26	445.5	10.1	595	22	AAAG84511	Human oestrogen re
27	445.5	10.1	595	22	AAAG84512	Human oestrogen re
28	445.5	10.1	595	22	AAAG84513	Human oestrogen re
29	443.5	10.0	595	22	AAAG84508	Human oestrogen re
30	443.5	10.0	595	22	AAAG84514	Human oestrogen re
31	442.5	10.0	595	8	AAAP70543	Human oestrogen re
32	442.5	10.0	595	20	AAV33506	Human estrogen re
33	427.5	9.7	582	22	AAAG78227	Lepomis centrarchi
34	427	9.7	457	22	AAAG61499	Protein encoded by
35	423	9.6	730	20	AAV04436	Rat RER beta-4 c10
36	421.5	9.5	422	22	AAAB61498	Protein encoded by
37	420	9.5	414	20	AAW98127	Rat oestrogen rece
38	417	9.4	530	18	AAW33215	Human oestrogen re
39	417	9.4	530	20	AAW97858	Human oestrogen re
40	417	9.4	530	22	AAE10457	Human estrogen rec
41	417	9.4	530	22	AAV27322	Human oestrogen re
42	417	9.4	530	22	AAAB60549	Human oestrogen re
43	417	9.4	548	20	AAV07270	Human oestrogen re
44	416	9.4	549	20	AAV04434	Murine MER beta-1
45	415	9.4	93	17	AAAP90714	DNA-binding domain

## ALIGNMENTS

RESULT	1	AAV21622	standard; protein; 984 AA.
ID	AAV21622		
XX	AAV21622:		
AC	AAV21622:		
XX			
DT	11-AUG-1999 (first entry)		
XX			
DE	Ligand binding domain of nuclear receptor hMR.		
XX			
KW	Thyroid hormone receptor; aromatic compound; ligand binding domain;		
KW	alpha-glycerophosphate dehydrogenase; cardiac; obesity; triglyceride;		
KW	plasma cholesterol; anti-hypertiglycerideemic; atherosclerosis; GPDH;		
KW	thyroid hormone replacement therapy; nuclear receptor.		
XX			
OS	Homo sapiens.		
XX			
PN	W0926966-A2.		
XX			
PD	03-JUN-1999.		
XX			
PF	25-NOV-1998; 98WO-US25296.		
XX			
PR	26-NOV-1997; 97US-0980115.		
XX			
PA	(REGC ) UNIV CALIFORNIA.		
XX			
PI	Aprilletti JW, Baxter JD, Pletierick RJ, Kushner PJ;		
XX	Scanlan TS, Shiau AK, Wagner RL, West BL;		
XX	WPI; 1999-357810/30.		
PT	Modulating activity of a thyroid hormone receptor		
XX			

PS Disclosure; Fig 3A-R; 447pp; English.

The invention relates to a method for modulating activity of a thyroid hormone receptor that comprises administration of an aromatic compound which fits spatially and preferentially into a thyroid hormone ligand binding domain. The aromatic compound (of a specified formula) can be used to increase alpha-glycerophosphate dehydrogenase (GPDH) levels, at levels which do not significantly modify cardiac GPDH levels and are indicated in the treatment of obesity. The compound also lower total plasma cholesterol and triglyceride levels and can be used as anti-hyperlipidaemic agents. The compound may also be used for treating atherosclerosis and may be indicated in thyroid hormone replacement therapy in patients with compromised cardiac function. Sequences AA121521- 636 amino acid sequences of ligand binding domains of several members of the nuclear receptor superfamily.

Sequence 984 AA;

Query Match	99.2%	Score 4385;	DB 20	Length 984;
Best Local Similarity	100.0%	Pred. No. 9.3e-266;		
Matches 837; Conservative	0;	Mismatches	0;	Gaps 0

[illegible]

Db 721 talvpqistisraltspvwm leniepeivyaygsskptdaenllstlnrlagkqmiqy 780

Qy 781 VKMAVLEPGFNLPLEDOITLIQSWMCSSFALSMMSKYHTNSQFLYFAPDLVENE 837

Db 781 vkwkvlpqfnlpdeditliqysmncsfalswrsyhtnsqflyfapdlvne 837

## RESULT 2

ID AAP80927 standard; protein; 984 AA.

AC AAP80927;

DT 29-DEC-1990 (first entry)

Sequence of the human mineralocorticoid receptor (hMR) -

**KW** Hormone receptor; hormone-binding; transcription activation.

... Homo sapiens

PN W08803168-A.

PD 05-MAY-1988.

PF 23-OCT-1987; 87WO-US02782.

20-OCT-1987; 87US-0108471.

PA (SALK ) SALK INST FOR BIOL STUD.

PI Evans RM, Weinberger CA, Hollenberg SM, Giguere V,

\*\*\*  
DR WPT; 1988-133242/19.

DR N-PSDB; AAN80920.

PT Recombinant DNA encoding hormone receptors -  
PT comprising glucocorticoid, mineralocorticoid, thyroid hormone  
PT and novel hormone receptors

PS Claim 17; Fig IV-2(B)-1 and -2; 243pp; English

DNA encoding hormone receptors and the hormone receptors themselves are claimed. The DNA can be used to make the hormone receptor proteins and functional modified forms in quantities not previously possible. The receptor proteins can be used to screen cpts. for receptor-agonist or receptor-antagonist activity. They can also be used in diagnostic assays

... Sequence 984 AA;

Query Match	99.08%	Score 4377;	DR 9;	Length 984;
Best Local Similarity	99.98%	Pred. No. 3e-265;		
Matches 836; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0

QY	1	MEKCTYHSLPELDIMERKRWGSOAVPESSISGLPEREDDENNYMEITVWSCVSGAIPENST	60
Db	1	metktyhslpeyliderrwgvsgavessl9pcercdennymeivwscvsgaipnnt	60
QY	61	QGSSEKOEELPCLOODNNRPGILTSDIKTELESKEUSATVABSMGLYMDVRDADYSTE	120
Db	61	qgsssekqellpclpqdnnrpgiltsdiktelseekelsatvaeemgilymvsyvdadyste	120
QY	121	QONOGSMSPAKITTYONVEOLVKEYFGNGHRRSTSLSCVNTPLRSFMSGSGSVNGGVRAI	180
Db	121	qonqgsmspakitygneqlxkyfgnghrpslscvntplrfsmgsagsvngvrra	180
QY	181	VKSPIMCHCKRSSVCSPLNMTNNSVCSFAGISVSSSTAARESPFVHSPITOGPRLTCSN	240
Db	181	vkspimchcksspsvcsplmtnnsvsfspaglnsvsstasfvsfpvhspliqgclrltcsn	240
QY	241	AENRGSRSHSPHAAENVGSPSLSPSSMSKSSISDPHSHCVKSPFVSSPNVTLRSSVSP	3000

```

Db 241 aenrgrshpahasnvgspslspslsmksaispsphcswkspvsnvnlrrsvvssp 300
QY 301 ANINNSGCSVSSPSNTNNRSTLSSPAASTVGTSCSPVNNAFSTYASGTSAGSSTLRVYP 360
Db 301 aannscsvsspsntnnrslsspaastvgtscspvnnafstysagtsagssltlrdivp 360
QY 361 SPPTOEKGADEVPPKTEEVESAINSGVQLNTVOYIKPEPDGAFSSCGSGSKINSND 420
Db 361 spptqekgaevppfkteevesaingsvtqnlivvyikpepdgaftsscgsgskinsnd 420
QY 421 SFSVPTRKQSTKHSCTGTFKGNPTVNPFFMDGSYFSFMDKDYXSLSGILGPYPVGF 480
Db 421 sfsivptkqgstkhscsgtsfkgnptvnpffmdgsyfsfmdkdyxslsgilgppvpgf 480
QY 481 DGNCEGSPFVGTIKQEPDSDGYPEASIPSSALVGNVSGGSPHYRIGAGCTISLSRSAR 540
Db 481 dnceegsfvgtikqepddgsyypaasipssalvgnsggsphyrigagctislsrsar 540
QY 541 DQSFQHLSSFPVNTLVESKSHGDLSSRRSDGYPVLEYIPENVSSSTLRVSTGSSRPS 600
Db 541 dqsfqhlssfpvntlvesskshgdlssrrsdgyvpvleyipenvssstlsvstgssrps 600
QY 601 KICLVCGDEASGCHYGVTCGSCVFPRRAVEGQHNVLCAGRNDCTIDKIRKNCPCARL 660
Db 601 kiclvcgdeasgchygvtcscvfkkravegqhnylcagrndctidkirkncpcarl 660
QY 661 OKCLQAMNIGARKSKLGLKGIHEQPOOQPPPPPPQSPBEGTTYIAPAKKESVN 720
Db 661 okclqamnlgarksklglkgiheeqpqpppppppspeeqtlylapakepsvn 720
QY 721 TALVPQSTISRALTSPVAVLENIPEEIVYAGDSKPPDAEMILSTLNLAGKOMIOY 780
Db 721 talvpqstisratlspvavlenipeeivayagdsckppdaemilstlnlagkomioy 780
QY 781 VKMAKVLPGFKNLPLEDQITLIOYSNMCLSFALSMRSYKHTNSQPLFYFAPDLVENE 837
Db 781 vkwkvlpfgknlpledqitlioyssmclsfalsmrsykhntnsqplfyfapdlvne 837

RESULT 3
AAP80919 standard; protein: 777 AA.
XX
AC AAP80919;
XX
DT 29-DEC-1990 (first entry)
XX
DE Sequence of the primary protein sequence of human glucocorticoid
XX receptor (hGR).
XX
KM Hormone receptor; hormone-binding; transcription activation.
XX
OS Homo sapiens.
XX
PN M08803168-A.
XX
PD 05-MAY-1988.
XX
PF 23-OCT-1987; 87WO-0502782.
XX
PR 20-OCT-1987; 87US-0108471.
XX
PA (SALK ) SALK INST FOR BIOL STUD.
XX
PI Evans RM, Weinberger CA, Hollenberg SM, Giguere V;
XX
DR WPI: 1988-133242/19.
XX
DR N-PSDB; AAN80916.
XX
PT Recombinant DNA encoding hormone receptors -
XX comprising glucocorticoid, mineralocorticoid, thyroid hormone
XX and novel hormone receptors
XX

```

```

PS Claim 24; Fig I-2(1) to (2); 243pp; English.
XX
CC DNAs encoding hormone receptors and the hormone receptors themselves are
CC claimed. The DNA can be used to make the hormone receptor proteins and
CC functional modified forms in quantities not previously possible. The
CC receptor proteins can be used to screen cdfs. for receptor-agonist or
CC receptor-antagonist activity. They can also be used in diagnostic assays.
XX
SQ Sequence 777 AA:

Query Match 19.4% Score 856; DB 9; Length 777;
Best Local Similarity 35.0% Pred. No. 3.4e-45;
Matches 239; Conservative 83; Mismatches 212; Indels 148; Gaps 25;

QY 248 SHSPAHASNVGSPSLSSPSLSSKSSISBPSHCSVSPVSPNNVTLRSSVSPANNINNR 307
Db 6 sltpgreenpsvslagerdymdfyklrgatavkvaassps-----lavsgdsxqtr 60
QY 308 CSVSSPSTNNRS---TLSSPAASTVG-----SICSPVNNAFSTYASG---TSAGSSTLR 356
Db 61 llydfpkgsvnaeqpdlksavslsmglymgelctkvmgnlgrfpqgqslssgetdlk 120
QY 357 DVVPS-----PPTOEKGAQ-----EVPFKTEEVESAINSGVQLNTVOYI 398
Db 121 lleeianlnrstvpenpkasastavsaaptekefkthdvaseqghlkq----- 173
QY 399 KPEPDGAFSSSCLCGNSKI--NSDSFSY-----PIKQSTYHSCGSGTFKGNPT 446
Db 174 -----lgtngnkvlyltdqstfdlqldeffssgsqpketneapwrsdliidenc 224
QY 447 VNPPFFMDGSYF-----SFMDKDYX--SLSGILGPYPGPDNCE 485
Db 225 lsplageddsslfgnsgnedckpiliptkpkixdngqlvlspsnvrlpvyv-----kte 279
QY 486 GSGC-----PYGIRKQEPDSDGYPEASIPSSAIVG-----VNSGGQSFHYRIGA 529
Db 280 kedfielctpgvikqe-klgtvycgaafpganliqgnksalsvghvetsgqmhlydm-- 336
QY 530 QGTISLSRSARDGQFQHLSSFPVNTLVESW---KSHGD--LSSRRSDGYPVLEYIPBNV 584
Db 337 -ntaslsqg-qdqk-plfnvlpipvgsewnrcqgsqddnltslgltnfpgrvfsnuy 393
QY 585 SSSSTLR-----SVTGGSS-RESKITLVCGDEASGCHYGVTCGSCVFPRRAVEGQH 635
Db 394 sspsmrvdvspspsstactatgppkcltvcdeasgchygvtcscvfkkravegqh 453
QY 636 NYLCAGRNDCTIDKIRKNCPCARLOKCIAGMNLGARKSKLGLKGIHEQPOOQPP 695
Db 454 nylcagrndctidkirkncpcarykclqagmnlgaarktkk--klygi-----qgat 504
QY 696 PPPPPOSPEBGTYYIAPAKKESVNTALVPLQSTISRALTSPVAVLENIPEEIVYAGD 755
Db 505 tgvsgetsepngnktilvapilpq-----lptlvsllveiepyaygd 549
QY 756 SSKPDTAENLSTLNRLAGKOMIOYVWAKVLPGEKNLPLEDQITLIOYSNMCLSFALS 815
Db 550 ssvpdstwrmittlmlygrivgaavkwakapjfrnlhiddqmtllygswfmfatalg 609
QY 816 WRSYKHTNSQPLFYFAPDLVENE 837
Db 610 wrsyrgsaanllcfapdlilne 631

RESULT 4
AAM44700 standard; protein: 777 AA.
XX
AC AAM44700;
XX
DT 12-MAY-1998 (first entry)
XX
DE Mutant nuclear glucocorticoid receptor I747T.
XX

```





```

Db      403 qgq|qlsge|dfr|leesi----- 422
QY      182 KSPIMCHEKSPVCSPLNMTTSSVCSPPAGINSVSTTASFGSPFVHPSPITQGTPLTCSRNA 241
Db      423 -----anhrstcspe-----npksslsatgcat|pteket|pk-thdassseq 463
QY      242 ENRGSRSHSPAHASNVGSPPLSSSMKSSISSPSHCSVKSPVSSPNNVTLRSSVSPA 301
Db      464 qurksqt-----gtngsgsvk|ypltdqst|fd|lk-dlefsagpspkd|res|pwsrd|ll|de 517
QY      302 NNNNSRCVSSP-----SNTNNRSTLSSPAASTVGSICSPVNNAFSTASGSAGSSTLRD 357
Db      518 nllsp|ageddp|fl|egntned-----ckp----- 542
QY      358 VVSPDTEKGAQOEVPFKTEVESALISNGVTLQNLIVQYIKRPDGAFASSSCUGANSKI 417
Db      543 -ll|pdtk-----pk|kdt-----gdt|l 560
QY      418 NSDSFSVP-|KQESTKSHSCGTSFKGNPTVNPFPFMGSIFFSMDKDYISLSGILGPP 476
Db      561 sspsva|lpq|y|ktek-----dd|elc----- 582
QY      477 VPFEGNGEGSGFPVGIKQEPDDGSYPEASIPSSAIVG-----VNSGGQSPHY 525
Db      583 tpgv-----lkge-k|l|pvy|qaa|fstg|n|l|gkmsa|sv|ngvst|sgq|my|hy 629
QY      526 R|GAGCT|SLSRARDQSFQHLSSFPVNTLVESWK-----SHGDLs-----SRR 570
Db      630 dm-----ntas|lsq|-gdqk-pv|fnv|p|p|p|vgsenwrcqsgeda|l|a|g|n|f|p|g|v|f 684
QY      571 SDGVPVLEIPENNVSSSLRSVSTGSSRPSKICLVCGDEASCHGVYTCGCKYFFRRA 630
Db      665 snqyspmp|rvpsv|spssaa|tgp--p|k|c|l|v|c|d|e|a|s|g|h|y|l|c|g|e|c|k|f|f|k|ra 742
QY      631 VEGQHNYLCAGRNDCI|DKIRRNCPACR|LQCLQAGNMLGARKSKLTKLGIHEEPQ 690
Db      743 vegq|ny|l|c|a|g|n|d|c|l|k|l|r|k|n|c|p|a|c|y|k|c|l|q|a|g|m|l|e|a|r|k|k--k|k|y|q|a|t|a|g 800
QY      691 QQQPPPPPPPPQSPREGT|TYIAPAKEPSVNTALVPOLSTISALNPSPVME|EN|E|P|V 750
Db      801 vsq-----d|t|s|e|n|p|k|t|y|p|a|l|p|q-----l|p|t|v|s|l|l|e|v|e|p|l 837
QY      751 YAGYDSKPD|TAEN|L|L|STL|RLAG|KQMTQVYKMAKVLPGFKMLPLEDOITL|IYQ|G|M|C|L|S 810
Db      838 yag|y|d|s|v|p|d|s|a|w|r|l|m|t|l|m|l|g|r|q|v|a|a|v|k|a|k|a|l|g|l|r|h|l|d|d|q|m|l|l|q|y|s|m|f|m 897
QY      811 SFALSRSYKHTNSQFLYFAPDLVENE 837
Db      898 afa|l|q|w|s|r|y|g|s|g|n|l|l|c|f|a|p|l|l|n|e 924

RESULT 7
AAV97297
ID      AAV97297 standard; Protein; 933 AA.
AC      AAV97297;
XX      03-JAN-2001 (first entry)
DE      Human progesterone receptor B-form.
XX      Recombinant DNA; gene therapy; hormone responsive element;
KW      transgene; HRE; haemophilia; clotting factor IX; vaccine;
KW      regulation; breast cancer; ovarian cancer; prostate cancer;
KW      von Willebrand disease; cystic fibrosis; hormone; receptor; human;
KW      blood.
OS      Homo sapiens.
XX      WO200049147-A1.
PN      24-AUG-2000.
PD

```

```

XX      18-FEB-2000; 2000WO-EP01368.
PF      19-FEB-1999; 99DE-1007099.
XX      19-FEB-1999; 99US-0120848.
PR      19-FEB-1999; 99US-0120848.
XX      (THER-) THERAGENE BIOMEDICAL LAB GMBH.
PA      Hauser-funke C;
XX      WPI; 2000-549273/50.
XX      N-PSDB: AAA53851.
DR      Novel nucleic acid construct useful in gene therapy comprising an
PT      hormone responsive element and transgene in which the hormone
PT      responsive element is not functionally linked to the transgene
PS      Disclosure: Page 92-95; 100pp; English.
XX      New nucleic acid constructs are described which comprise an hormone
CC      responsive element (HRE) and a transgene (T). Alternatively the
CC      nucleic acid construct, comprises at least one HRE and a transgene;
CC      where one of the HREs is not functionally linked to the transgene;
CC      The constructs can be used to up-regulate or down-regulate target
CC      genes and for the delivery of vaccines. The constructs preferably
CC      comprise a transgene which encodes a protein which is lacking in a
CC      variety of genetic disorders or involved in conditions related in
CC      inappropriate responses to hormones, for example hormone-dependent
CC      cancers such as breast, ovarian, and endometrial cancers and prostate
CC      cancer. The transgene may also be used to replace a defective gene
CC      resulting in such genetic disorders as haemophilia, von Willebrand
CC      disease, and cystic fibrosis. Vectors comprising these constructs
CC      where the transgene is human clotting factor IX can be used for
CC      treating blood clotting disorders such as haemophilia A or B on
CC      administration to an organism or to a cellular system. The constructs
CC      have applications in gene therapy for treating haemophilia when the
CC      transgene encodes a clotting factor such as clotting factor IX. The
CC      advantage of this system is that the hormone-hormone receptor complex
CC      contains a hormone receptor that becomes activated after binding of
CC      its specific hormone. The hormone receptor in the activated state is
CC      able to recognise and bind to its specific hormone responsive
CC      element. The presence of the hormone responsive element on the
CC      nucleic acid carrying a transgene encourages binding of a
CC      hormone-hormone receptor complex. Thus the activated hormone receptor
CC      acts as a link between the nucleic acid carrying the transgene and the
CC      hormone known to interact with the cell membrane.
XX      Sequence 933 AA:
SQ
Query Match 18.2%; Score 806; DB 21; Length 933;
Best Local Similarity 29.1%; Pred. No. 5,8e-42;
Matches 248; Conservative 95; Mismatches 231; Indels 278; Gaps 33;
QY      191 SPSVCSPLNMTTSSVCSPPAG-----INSVSTTASFGSFPVYHSITGT--PLTG---SPNA 241
Db      20 spevg|spl-----l|or|paa|g|f|p|g|s|q|s|d|t|l|p|e|v|a|l|p|s---l|d|g|l|f|p|c|q|g|d|b|s|d 71
QY      242 EN-----RGSRSHPAHASNVGSPPLSSP-----LSMKSSISSPSHCSVKSPV 285
Db      72 ekt|q|q|s|l|d|e|g|a|y|s|t|a|e|a|t|r|g|a|g|s|s|p|p|e|k|d|s|g|l|d|e|v|l|d|l|a|p----- 121
QY      286 SSPNNVTLRSSVSPANTNNRCSVSS-----PSNTNNRSTLSSPAASTVGSICSP 336
Db      122 sgpg-----gsq|ps|p|a-----c|e|v|t|s|w|c|l|f|p|e|l|p|e|d-----p|p|a|p|a|t|q|v|l|s|p 163
QY      337 VNNAFSYTASGTSAGSSTLRDVP--SPDTQ-----EKAQOEVPFKTEVESGA 383
Db      164 lmsr-sgckv|g|d|s|g|t|a|a|h|k|v|l|p|g|l|s|p|a|q|l|l|p|a|s|e|p|h|w|s|g|a|p|k|p|s|q|a|a|v|e 222
QY      384 ISNGVTLQNLIVQYIKRPEDGAFSSSCUGANSKI-----NSDSFSVP----- 426
Db      223 eed|g|s|e|s|e|s|a|g|l|l|k|y|k|p|r|a|l|g|a|a|g|g|a|a|v|p|p|g|a|a|g|v|a|l|v|p|k|e|d|s|f|s|a|p|r|v|a|l 282

```

OY	IKOES-----	THSGSGTSFKG-----	443
Dd	283 veqdapamgrslatltvmdflhvplllplnhallaarltrqlledesydggaqaasaafap	: : : :	342
OY	444 --NPTVMPFP-----FMDGSYFSFMDDKD-----	:	465
Dd	343 rrsppcaastprwagvdfrdcceypprdaeckdayllyadfdqpraalkikeeeggeaaasrrsr	: : : : : :	402
OY	466 YYSLSGI-----LGPVP-----	GFDGNC--	484
Dd	403 sylvaganaapaafdrfpdypppprlpratrpsrgaeavtaapaasvsasssgstlecll	: : : : : :	462
OY	485 -----ECSRGPVIGIKQEPDGDGYRPEASIRPSAIVGVNNGCGSFHY-RIGAGTIS	534	
Dd	463 ykaeaqpqqgpfarpckkapagsagccllprdgiprstsaasaaaapaalypalglnlbpq	522	
OY	535 LSRAPDOSFOHLSSFPVMTVLVESMKSHGDLSSRRSDGYPVLEYI-PENVSSTLRSVS	593	
Dd	523 lgygaavlk-----eglpqvyp-----pylnylrpdseasgspq-y	557	
OY	594 TGSSRPSPKICLVGCDEASGCHYGVTTCSCRYEFKRAVEEQHNYYLCAGRNDCTIDKRKK	653	
Dd	558 sfeslpgqliclcgdeasgchvgyltcgsckvfkramegqhnylcaagrndcivdkirrk	617	
OY	654 NCPACRIQCKLOAGAMNLGAARSKSKLKGLKLINE-EGPQQOOQPPPPPPOQSDEEXTTYIA	712	
Dd	618 ncpacrlrkcgcgaawlgvqkfkfknfvrvraidaavalpqrlgvynoesqalsqrftl--	675	
OY	713 PAKEPSVTALVPLQTLSTISNALTPSPMVWLENTEPELIAVGYSKSPPDAEMNLSTLNRL	772	
Dd	676 ---spgqdilqilppl-----inlmislepdiyaghnonckrtpdsssltslnql	721	
OY	773 AGKOMIOYVKMAKVLPGEFKMLPLEDOITLLIQYSWMCLSSFALSWSRSKHTNSQFLFYAPD	832	
Dd	722 gerqlisvkwkskelpgfrnlhdidqtliliqyswmslmwfglygrvyzkhvsgqmlylapd	781	
OY	833 LVFNELLARVRE 844		
Dd	782 ilne-qrmke 791		
 RESULT 8 AAAY21621 ID AAY21621 standard; protein; 933 AA. XX AC AAY21621; XX DT 11-AUG-1999 (first entry) XX DE Ligand binding domain of nuclear receptor hPR. XX KW Thyroid hormone receptor; aromatic compound; ligand binding domain; RW alpha-glycerophosphate dehydrogenase; cardiac; obesity; triglyceride; KW plasma cholesterol; anti-hypertriglyceridaemic; atherosclerosis; GPDH, KW thyroid hormone replacement therapy; nuclear receptor. XX OS Homo sapiens. XX PN MO9926966-A2. XX PD 03-JUN-1999. XX PF 25-NOV-1998; 98MO-US25296. XX PR 26-NOV-1997; 97US-0980115. XX PA (REGC ) UNIV CALIFORNIA. XX PI Apriletti JW, Baxter JD, Fletterick RJ, Kushner PJ; PI Scanlan TS, Shiau AK, Wagner RL, West BL; XX DR WPI; 1999-357810/30.			

XX		Modulating activity of a thyroid hormone receptor
PT		
PS		
XX		Disclosure; Fig 3A-R; 447pp; English.
CC		The invention relates to a method for modulating activity of a thyroid
CC		hormone receptor that comprises administration of an aromatic compound
CC		which fits spatially and preferentially into a thyroid hormone ligand
CC		binding domain. The aromatic compound (of a specified formula) can be
CC		used to increase alpha-glycerophosphate dehydrogenase (GPDH) levels, at
CC		levels which do not significantly modify cardiac GPDH levels and are
CC		indicated in the treatment of obesity. The compound also lower total
CC		plasma cholesterol and triglyceride levels and can be used as anti-
CC		hypertriglyceridemic agents. The compound may also be used for treating
CC		atherosclerosis and may be indicated in thyroid hormone replacement
CC		therapy in patients with compromised cardiac function. Sequences
CC		AAV1621- 636 amino acid sequences of ligand binding domains of several
CC		members of the nuclear receptor superfamily.
XX		
SQ	Sequence	933 AA:
Query Match	18.1%; Score 801; DB 20;	Length 933;
Best Local Similarity	29.5%; Pred. NO. 1.2e-41;	
Matches	253; Conservative	95; Mismatches 221; Indels 288; Gaps 37
Dn	191 SPSPCVSLMTMTSSVCSPAG---- <td>        :       :       :       :       :</td>	:       :       :       :       :
Dn	20 spvsgspl-----lcrpaagpfpsqgtsdltlpveasiprs---ldglfllprpcggqdped 71	:       :       :       :       :
Dn	242 EN-----RGSRSHPAHASNVGPSLSSP-----LSSMKSSISSPSHCYKSPV 285	:   :   :         :       :       :       :
Dn	72 ektdqqsldvdgystraetraergagsssppekdsjldvidtllap----- 121	:       :       :       :       :
Dn	286 SSPNWTLRSSVSSPAININNSRCYSV-----PSTNNKRSLTSSPAATSVSICSP 336	:       :       :       :       :
Dn	122 sgpgy-----gsqgsppa-----cevlswclfgelped-----ppaatqtgrvls 163	:       :       :       :       :
Dn	337 VNNAESTRASCTSGASSSTRADVPV--SPDRT-----EKGAOEPPFP----KTE 378	:   :   :         :       :       :       :
Dn	164 lmsr--sgckvydsgstlaahkxvlprglsparglllpasespiwsgapyvkpsqaawe 222	:       :       :       :       :
Dn	379 EWESATISNGVTQLNIYOYIKPEP-----DGAEFSSC-----LGNSKI--NSDSFSV 425	:   :   :         :       :       :       :
Dn	223 eedseseesagpl-----lkqkpralggaaggaaacppgaagvalypkedsrfsa 277	:       :       :       :       :
Dn	426 P-----IKQDS-----TKHSCTGSTFKG----- 443	:   :   :         :       :       :       :
Dn	278 pvalavegdadmaprgprslattvmgfihylplnlhaallaatrqlledesydgagaas 337	:       :       :       :       :
Dn	444 -----NFTVMPFP-----FMDSGYSEFPMDDKD----- 465	:   :   :         :       :       :       :
Dn	338 afaprltscsaascrpavaygdfrdcayppdaepkddayplysdfqpalklikeegaeas 397	:       :       :       :       :
Dn	466 -----YLSLSGI-----LGPVP-----GFD 481	:   :   :         :       :       :       :
Dn	398 arsprrsyilvaganaapaafdfpdlpprpplrptatprgeaarvlaapaasaavsassgst 457	:       :       :       :       :
Dn	482 GMC-----EGCGPFVGITKOEPDDGSIYPENASIPSSAIIVGVNSGGOSFHV--RIGA 529	:       :       :       :       :
Dn	458 leclillykaegappqgpfafappockarpagsacllprdiglpstsaasaagaapalypalg 517	:       :       :       :       :
Dn	530 QOTTILSRARROOSTQHLLSPFPVNTLVESMKSMSHDDLSSRRDGLPVLEYI--PENVSSST 588	:       :       :       :       :
Dn	518 nglpqlygqaavlk-----eglpyvp-----pylnlylrpdseaaqs 554	:       :       :       :       :
Dn	589 LRSVSTGSSRPRIKLAVGDDEASGCHYGVTGSCCKVEFFKRAVEGOHNHYLCGRNDCIID 648	:       :       :       :       :
Dn	555 pq--ysfeelppkiclicldegdeasghyvtlcgscokffkramegqhnylcaqrndciivd 612	:       :       :       :       :
Dn	649 KTRRNKNPCACRLQCLQAGMNIGAKSKKLGKLGKIH-EQPQQQQPPPPPPOSPPEG 707	:       :       :       :       :
Dn	613 klrtknpacactrlckcqqgmviygtrkfkkfnkvrvvraidaavalbpqplgvpnsegalsqr 672	:       :       :       :       :

```

OY 708 TTYIAPAEPSVNLTAPOLSTISRALRPSPVMYLENTEPEIYVAGXDSSKPDIAENLTS 767
Db 673 tft-----spgqdiqlippl-----inllmslepdyIyaghnctkpcussllt 716
OY 768 TLNRLAGKOMIQVYKMAVVLPGFKNLPLEDOITLIQYSMCLISFPALSMRSYKHTNSQFL 827
Db 717 sinqlgeqgllslsvkwskslpgfrnlhhdqdlftllqyswmslmvtglgwrsykhvsgqml 776
OY 828 YFAPDPLVFNELLIARYE 844
Db 777 yfapdlilne--qrmke 791

RESULT 9
AAP93110
ID AAP93110 standard; protein; 902 AA.
XX
AC AAP93110;
XX
DT 19-MAR-1990 (first entry)
XX
DE Rat androgen receptor.
XX
KW Rat androgen receptor; monoclonal antibody; pIoyclonal antibody; cancer.
XX
OS Rattus rattus.
XX
PN W08909791-A.
XX
PD 19-OCT-1989.
XX
PF 13-APR-1989; 89WO-US01548.
XX
PR 14-APR-1988; 88US-0182646.
XX
PA (UYNC-) UNIVERSITY OF NORTH CAROLINA.
XX
PI French FS, Wilson EM, Joseph DR, Lubahn DB;
XX
PI WPI: 1989-324206/44.
XX
DR N-PSDB: AAN91773.
XX
PT DNA encoding androgen receptor protein - useful for transforming
XX
PT eukaryotic hosts for protein expression and subsequent antibody prodn.
XX
PS Disclosure: Fig. 5; 41pp; English.
XX
CC Androgen receptor protein (AR) is used to produce mono- or poly-clonal
XX
CC antibodies. These are used for the detection and quantification of AR in
XX
CC the presence of endogenous androgen, as androgen will not interfere with
XX
CC binding. They may be used in assays to determine and quantify cellular
XX
CC distribution of AR in tumour tissue, and are esp. useful for evaluating
XX
CC prostate cancers to determine responsiveness to androgen withdrawal
XX
CC therapy.
XX
SO Sequence 902 AA.

Query Match 17.2%; Score 758.5; DB 10; Length 902;
Best Local Similarity 30.1%; Pred. No. 5, 2e-39;
Matches 232; Conservative 83; Mismatches 208; Indels 249; Gaps 26;

OY 231 QGTPLTCSNAEKGRGRSHSPAHASVWGSPILSSPLSMKSSIISSPPSHCSVKSVPSPNN 290
Db 68 qqbhedgsqbahrlgttylalee-----qqpsqgqsaseghpsegclpepqaatapy 121
OY 291 VYLRSSVSSPANINNRGCVSSPSNTNNRSTLSPASTVGSICSPVYNAFSTYASGTA 350
Db 122 kqlpgqppapqdqds-----aapstslilpg-----tfpglss 155
OY 351 GSGTLDVYVPSPT-----QEKGAQEVPPKTEVEFSALISNGVTGOLNIVQYI 398

```

Dd	156	csadtkdlilseaqcmmqllqqgqqqqqqqqqqqqqqqqqqvleegsssvrrar-----	208
Qy	399	KPEPDGAFSS---SCLGNSKINSDS-----SFSPVPIKOSTKHSCSGTGFKN---444	
Dd	209	--eatgapssakdsleylgnstll--sdasakejckavsvsmqigvealehlspgqllrgdcmy	265
Qy	445	---PTVMFPF-----FMDGSYFSFMDDKKDYVSYLSGLIGPVPVPGFDNCCEG	486
Dd	266	asl1ggppravirpcraplaeekslsldcegbgkylteeaaesfkgdyakklgeeslgcsg	325
Qy	487	S-----GPPVGIKOE------497	
Dd	326	sseagsgtllelpsllsyksagvadeaaaaynrdyyflfpialsqpphpprptpharixl	385
Qy	498	----DDGS-----TYPEASITPSAIVGVNCS-----QGSH-----YRI	527
Dd	386	enpsdysgsawaanaaqcrtygdaslhhgsvagpsctsgspataasswhltftaeegqlyp	445
Qy	528	GAGGTISLRSRA-----RDSFOHLS-----FP-----PVNTLVES-559	
Dd	446	ggggggsspsdaagrvapygyrtcrpqglasgedfsaseewvpqgvvnrvrpypscvkse	505
Qy	560	---WKS-----HGD--LSRSRSDGYVLEIETPENVSSTSLRSVTSGRSRSKICINOGDE	609
Dd	506	mqrwmenyvsppymdrlnlstcdhvrlpldlyfr-----Pktclilegde	548
Qy	610	ASGCNYGVVTGSCSCVFEPKRRAVEGOHNLTCAGRNDCTIDKITRRKNCPACRLQKCLAGMN	669
Dd	549	asgcnygalitgscvcvfkkraeqkkyklastrandctldkrtnknpscrltkcyeaamt	608
Qy	670	LGARSKSKIIGKLKKTGHNEOPOOOQPRPPRPPOQSPEGTTYIAAKRPSVNTALVPLST	729
Dd	609	Igaiklkiklynk-Iqee-----genesagsepds-----qkmt	643
Qy	730	ISR---ALTPEPWVLNIIEPELYAYGDSKSPDTAEMLSTLNRLAGKOMIQVYNMAK	785
Dd	644	vshiegycqpfllinvlaieipyvccahndngpdstaallssinejgerqlvnhvwkak	703
Qy	786	VLPFGKNLPLEDQTTLIOYSMWCISSFFALSMRSRKHTNSQFLTYAPDLVRE	837
Dd	704	alpgfnlhvdqmavlaqyswmglmvfwgrstfnvsnmlfyapdlvtne	755
RESULT_10			
AAP91006	ID	AAP91006 standard; protein; 902 AA.	
XX	AC	AAP91006;	
XX	DT	28-FEB-1990 (first entry)	
XX	DE	Rat androgen receptor DNA clone.	
KM	XX	Androgen receptor; TR2 polypeptide;	
XX	OS	Rat.	
XX	XX	Key	Location/Qualifiers
FH	FT	Region	1..902
FT	FT	/tag=	a
FT	FT	/product=	98 kD polypeptide
FT	FT	Region	170..902
FT	FT	/tag=	b
FT	FT	/product=	79 kD polypeptide
XX	PN	W08909223-A.	
XX	PD	05-OCT-1989.	
XX	PF	24-MAR-1989;	89WO-US01238.
XX	PR	30-MAR-1986;	88US-0176107.



PA (ARCH-) ARCH DEVELOPMENT CORP.  
 XX Liao S, Chang C;  
 XX WPI: 1989-309501/42.  
 DR N-PSDB; AAN91578.  
 XX New DNA encoding new androgen receptor and TR2 polypeptide(s) - able  
 PT to bind DNA, and derived antibodies, useful for receptor assay and  
 PT purification.  
 XX  
 PS Claim 8; Fig 3; 60pp; English.  
 CC The protein is used to raise antibodies for receptor assays and for  
 CC affinity purification.  
 CC The 98 kd product starts at the first Met codon; the 79 kd product  
 CC starts from the second.  
 XX  
 SQ Sequence 902 AA;

Query Match 17.2%; Score 758.5; DB 10; Length 902;  
 Best Local Similarity 30.1%; Pred. No. 5,2e-39;  
 Matches 232; Conservative 83; Mismatches 208; Indels 249; Gaps 26;

OY 231 OGTLTCSPAENGRSHSPAHASNNVGSPLSSPLSMKSSISSPPSHCSVKSPVSSPNN 290  
 DB 68 qghpedspqahlrqitgylalee-----qpsqqsaseghpsegclpegaatapg 121  
 OY 291 VTLSSVSSPANINNSRCSVSSPNTNNRSTLSPFASTVGSICSPVNNASTYASTGSA 350  
 DB 122 kglpqgpapdpqds-----aapstsllyp-----tfpglss 155  
 OY 351 GSSTLRDVVPSPD-----OEKGAQEVFPFTEEVESAINSGVTGQINTIYOYI 398  
 DB 156 csadikdliseaglmqllqq 208  
 OY 399 KPEPDGAFSS---SCLGNSKINSDS-----SFSVPIQESTKHSKSGTSFKGN--- 444  
 DB 209 -eatgapskskdsylqgnstl-sdsakelckavsvsmglvealehlspgeqlrgdcmy 265  
 OY 445 -----PTVNPFP-----FMDGSYFSFMDMDYSLSGILGPPPGDGNCEG 486  
 DB 266 asllggpavtrpccaplaeckglsldegpgkyteetaeystfkgyakglgeaglgsq 325  
 OY 487 S-----GPPVGIKQEP----- 497  
 DB 326 sseagsgtleipsalslykqavdeaaaygrdyntfplalsgpphphpphparikl 385  
 OY 498 ----DDGS-----YYPEASIPSSAIVGVNSG-----GGSF-----YRI 527  
 DB 386 enplldysawaaaaaqcrgyqlaahgsvagstgspatasswhlftfaeqqlygp 445  
 OY 528 GAOGTISLSRSA-----RDGSFOHLS-----FP-----PVMNLVSS- 559  
 DB 446 gggggsspsdaagvaygyrppqglasgeqdfsaesewyggvymrvpyspcvase 505  
 OY 560 ---WKS-----HGD---ISSRSDGYVULEYIPENVSSSTLSVSTGSSRPKICLVCGDE 609  
 DB 506 mgpmemygpygdmridstldhvlpidylyf-----pkktclcgde 548  
 OY 610 ASGCHGYVTCGSKVFPFKRAVEGQHTLCAGRDCCIIDTKRKNCPCRIQCLQAGMN 669  
 DB 549 asgchgyaaltcgsckvfkkaeegkqylcasrindctldkfrkncpsclrlkcyeaqmt 608  
 OY 670 LGARSKKLGKLGKIHGEQPOQOOPPPPPPPQSPPECTTYYIAPAKESVMTALVPOJST 729  
 DB 609 lgarlklklgnlk-lgee-----genssagspteds-----qamt 643  
 OY 730 ISR-----ALRPSVAVLENIEPELIVAGYDSSKPDTAENLSTLNLRAKGOMIOVVKAK 785  
 DB 644 vshlegyecqglflnvleaiepygvvcaghdnnpdsfaallsslnelgerqlvhnvkvak 703

OY 786 VLPQFKNLPLEDOITLTOYSMMCLSFALSMRSYKHTNQSOLYFAFDLVENE 837  
 DB 704 alpgrlnhvddqmaivlqyswmglmviamgwrsfluvsnrmllylapdlvine 755

## RESULT 11

ID AAR12224 standard; Protein; 902 AA.

AC AAR12224;

DT 20-AUG-1991 (first entry)

DE Rat androgen receptor.

KW rAR; DNA-binding protein; steroid hormone.

OS Rattus rattus.

FX Key Location/Qualifiers

FT Domain 540..610

FT /label= "DNA-binding domain

FT /note= "cysteine-rich"

XX W09107423-A.

XX 30-MAY-1991.

XX 19-OCT-1990; 90WO-US06015.

XX 17-NOV-1989; 89US-0438775.

XX (ARCH-) ARCH DEV CORP.

XX Liao S, Chang C;

XX WPI: 1991-178048/24.

XX N-PSDB; AAQ12002.

XX Androgen receptor and TR2 DNA binding proteins - DNA sequences

XX PT and antibodies for detection and quantification methods

XX PS Claim 25; Fig 3; 79pp; English.

XX This sequence was deduced from a cDNA clone isolated by screening

XX a rat ventral prostate lambda gt11 library in E.coli Y1090. The

XX sequence is very similar to that of human AR and in

XX CC the DNA-binding domain it is identical to that of hAR DNA-binding

XX CC domain. Homology comparisons with other known steroid receptors

XX CC indicate that rAR is more closely related to glucocorticoid,

XX CC mineralo-corticoid and progesterone receptors than to v-erb-A or to

XX CC receptors for oestrogen, vitamin D and thyroid hormones.

XX SQ Sequence 902 AA;

Query Match 17.0%; Score 753.5; DB 12; Length 902;  
 Best Local Similarity 30.3%; Pred. No. 1.1e-38;  
 Matches 229; Conservative 85; Mismatches 225; Indels 217; Gaps 24;

OY 231 OGTLTCSPAENGRSHSPAHASNNVGSPLSSPLSMKSSISSPPSHCSVKSPVSSPNN 290  
 DB 68 qghpedspqahlrqitgylalee-----qpsqqsaseghpsegclpegaatapg 121  
 OY 291 VTLSSVSSPANINNSRCSVSSPNTNNRSTLSPFASTVGSICSPVNNASTYASTGSA 350  
 DB 122 kglpqgpapdpqds-----aapstsllyp-----tfpglss 155  
 OY 351 GSSTLRDVVPSPD-----OEKGAQEVFPFTEEVESAINSGVTGQINTIYOYI 398  
 DB 156 csadikdliseaglmqllqq 208  
 OY 399 KPEPDGAFSS---SCLGNSKINSDS-----SFSVPIQESTKHSKSGTSFKGN--- 444







```

Db 228 stlsdnakelckavsvsmglgyvealehlspsgeqlrgdcmyapllgyppavrpptcaplae 287
OY 452 ----FMDGSYFSPMDKDYISLSGILGPPVPCPDG---NCEGS----- 487
Db 288 ckgsllddagstedtaey--spfkgytkqlgeslqcsaagsgtlelptslsl 345
OY 488 -----GFPVGINKQEP-----DDGS----- 501
Db 346 yksgaldeaaygsrdynfnlialagppppppphariklenpldygsawaaaaaqcr 405
OY 502 YYPEASIPSSAIVGVNSG-----GOSFHY----- 525
Db 406 ygdlaelhgagaagpgsgpsaasswhltlfaeeqlygpcg9999999999999999 465
OY 526 -----RIGAOGTISLSRSARDQSFQH-----LSSFP-PVNTLVES---- 559
Db 466 9999999999999999999999999999999999999999999999999999999 525
OY 560 WKS----HGD--LSSRRSDGYPVLEYIPENVSSSTLRSVSTGSSRPSKICICGDEASG 612
Db 526 wmdsypgpygdmrltarahvlpidyf-----pqktcllqgdaag 568
OY 613 CHGVVTCGSCVFFKRAVEGQHNYLCAGRNDCTIDKIRKNCPCACRLQCLQAGMNLGA 672
Db 569 chygaltcgsckvffkriaegkqkylcasrindctldkfrknopscrllrkyeagmtlga 628
OY 673 RKSCKLGLKGIHEEQPQOQPPPPPPPOSPEEGTTYIAPAKEPSVNTALVPOLSTIS- 731
Db 629 rk1kklgnlk-lqeegdaass-----ttspleelt-----qkltvash 663
OY 732 -----RALTPSPVWYLENIEPEIYVAGYDSSKPDFAENLSTLNRLAGQOMIQVYKMAK 785
Db 664 iegyecqalf---lnylealepvcagnnqpsfaalsslnelgerqlvhwkwak 720
OY 786 VLPGEKMLPLEDQITLIQYWMCLSSPALSWSRSYKHTNSOFLYFADPLVENE 837
Db 721 alpgffnlhvddqmvavlgyswmglmwflamgwrsftnvnsrmlyfapdlvfne 772

```

Search completed: September 13, 2002, 10:17:42  
 Job time: 106 sec

This Page Blank (uspto)

This Page Blank (uspto)

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 13, 2002, 10:15:56 ; Search time 25.39 Seconds

(without alignments)  
3197.932 Million cell updates/sec

Title: US-09-695-293-42

Perfect score: 4422

Sequence: 1 METKGYSHPGLDMERRMG.....FLYFADLYFNELLARVREG 845

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR-71:\*  
2: PIR1:\*  
3: PIR2:\*  
4: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4385	99.2	984	2	A29513	mineralocorticoid
2	3919.5	88.6	981	2	A41401	mineralocorticoid
3	865	19.6	771	2	A54273	glucocorticoid rec
4	856.5	19.4	776	1	SA4047	glucocorticoid rec
5	856	19.4	742	1	ORHUGB	glucocorticoid rec
6	856	19.4	777	1	ORHUGA	glucocorticoid rec
7	845.5	19.1	795	1	ORRTG	glucocorticoid rec
8	842	19.0	783	1	A25691	glucocorticoid rec
9	823	18.6	923	2	I53280	progesterone recep
10	814.5	18.4	758	2	SE60586	glucocorticoid rec
11	805	18.2	786	2	A35466	progesterone recep
12	804	18.2	923	2	A39596	progesterone recep
13	801	18.1	933	1	ORHUP	progesterone recep
14	800	18.1	930	2	A25923	progesterone recep
15	760	17.2	899	2	A35895	androgen receptor
16	758.5	17.2	902	2	B40494	androgen receptor
17	731.5	16.5	919	2	A39248	androgen receptor
18	730.5	16.5	910	2	A34721	androgen receptor
19	730.5	16.5	911	2	B34721	androgen receptor
20	718	16.2	848	2	JG0194	androgen receptor
21	644.5	10.4	586	1	ORXLE	estrogen receptor
22	641.5	10.3	589	1	ORCHE	estrogen receptor
23	456.5	10.2	595	2	I47140	estradiol receptor
24	452.5	10.2	166	2	S35795	androgen receptor
25	449.5	10.2	166	2	S35795	androgen receptor
26	442.5	10.0	595	1	ORHUE	estrogen receptor
27	442.5	10.0	701	2	SE4737	80k estrogen recep
28	440.5	10.0	599	1	ORMSE	estrogen receptor
29	436	9.9	600	1	ORRTE	estrogen receptor

30	417	9.4	530	2	JC5939	estrogen receptor
31	404	9.1	477	2	S71400	estrogen receptor
32	398.5	9.0	503	2	JW0046	estrogen receptor
33	395.5	8.9	620	2	T10423	estrogen receptor
34	393.5	8.9	521	2	A29345	steroid hormone re
35	377.5	8.5	701	1	S33709	DHR39-short protei
36	377.5	8.5	808	1	S33708	nuclear steroid/th
37	376	8.5	433	2	B29345	steroid hormone re
38	376	8.5	574	2	A17197	estrogen receptor
39	375.5	8.5	535	2	S58224	estrogen receptor
40	368	8.3	433	2	S58087	estrogen receptor
41	350	7.9	1043	2	T13733	PR2-F1 protein - f
42	340	7.7	601	1	ORMSN1	probable hormone r
43	338.5	7.7	598	2	A37251	probable nuclear h
44	338	7.6	628	2	JC2493	neuron derived orp
45	335.5	7.6	625	2	S71930	neuron-derived rec

#### ALIGNMENTS

```
RESULT 1
A29513
mineralocorticoid-receptor - human
N:Alternate names: aldosterone receptor
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 20-Sep-1999
C:Accession: A29513
R:Arriza, J.L.; Weinberger, C.; Cerelli, G.; Glaser, T.M.; Handelin, B.L.; Housman, D
Science 237, 268-275, 1987
A>Title: Cloning of human mineralocorticoid receptor complementary DNA: structural an
A:Reference number: A29513; MUID:87263386
A:Accession: A29513
A:Molecule type: mRNA
A:Residues: 1-984 <ARR>
A:Cross-references: GB:M16801; NID:g187460; PIDN:AAA59571.1; PID:g307166
C:Genetics:
A:Gene: GDB:MLR
A:Cross-references: GDB:120188; OMIM:264350
A:Map position: 4q31-4q31
C:Superfamily: unassigned erba-related proteins; erba transforming protein homology
C:Keywords: DNA binding; transcription regulation; zinc finger
F:601-880/Domain: erba transforming protein homology <ERBA>
F:603-623/Region: zinc finger
F:639-663/Region: zinc finger

Query Match 99.2%; Score 4385; DB 2; Length 984;
Best Local Similarity 100.0%; Pred. No. 1.7e-220; Mismatches 0; Indels 0; Gaps 0
Matches 837; Conservative 0; Mismatches 0; Indels 0; Gaps 0

OY 1 METKGYSHPGLDMERRMGVSQAVERSLGPRTDENNYMEIVNVCVGAIPNNST 60
    |||||||
DB 1 METKGYSHPGLDMERRMGVSQAVERSLGPRTDENNYMEIVNVCVGAIPNNST 60
    |||||||

OY 61 QGSSKEKQELLPCLODDNNRPGLITSIDIKTELESKELSAVSEGLVDSVRDADYSYE 120
    |||||||
DB 61 QGSSKEKQELLPCLODDNNRPGLITSIDIKTELESKELSAVSEGLVDSVRDADYSYE 120
    |||||||

OY 121 QONOGSGSPAKTYONVEOLVFYKGNHRPSTLSCVNPPLSFMSDGSVNGCVMAI 180
    |||||||
DB 121 QONOGSGSPAKTYONVEOLVFYKGNHRPSTLSCVNPPLSFMSDGSVNGCVMAI 180
    |||||||

OY 181 VKSPTMCHERKSPVSCSPLMTSSVCSFAGINSVSTTASFGSPVHSPITQGTPLTCSFN 240
    |||||||
DB 181 VKSPTMCHERKSPVSCSPLMTSSVCSFAGINSVSTTASFGSPVHSPITQGTPLTCSFN 240
    |||||||

OY 241 AENRGRSRSHPAHANSVGSPLSSSMKSSISSPSPHCVSPVSPNNVTLRSSVSP 300
    |||||||
DB 241 AENRGRSRSHPAHANSVGSPLSSSMKSSISSPSPHCVSPVSPNNVTLRSSVSP 300
    |||||||

OY 301 ANINNSRCSVSSPNTNNTSLSSPAASTVSGISCPVNNAFSYTASGTSAGSSTLRDVP 360
    |||||||
```

```
Db 301 ANINNSRCVSSPENTNNRSTLSSPAASIVGSIQSPVNNAFSTYAGTSAGSSTLRDUVP 360
Qy 361 SPPTQEGAEQVEPPTKEEVEBSAISNGVTGOLNIYOYIKPEPDCAFSSCLGSKINSND 420
Db 361 SPPTQEGAEQVEPPTKEEVEBSAISNGVTGOLNIYOYIKPEPDCAFSSCLGSKINSND 420
Qy 421 SSFSPVPIKQESTKSCSGTSFKGNPTVNPFPFMDGSYFSFMDKDYYSLSGILGPVPGF 480
Db 421 SSFSPVPIKQESTKSCSGTSFKGNPTVNPFPFMDGSYFSFMDKDYYSLSGILGPVPGF 480
Qy 481 DGNCEGSGFPVGIKQEPDDGSYPEASIPSSAIVGNSGSGSFHYRIGAOGTISLSRSAR 540
Db 481 DGNCEGSGFPVGIKQEPDDGSYPEASIPSSAIVGNSGSGSFHYRIGAOGTISLSRSAR 540
Qy 541 DQSFQHLSSFPVNTLVESKSHGDLSSRSDGYPLEYIPENYSSSTLRVSSTGSSSRP 600
Db 541 DQSFQHLSSFPVNTLVESKSHGDLSSRSDGYPLEYIPENYSSSTLRVSSTGSSSRP 600
Qy 601 KICLVGDEASGCHYGAVTGCSCVFFKRAVEGQHNILCAGRNDCTIDKIRKNCPCARL 660
Db 601 KICLVGDEASGCHYGAVTGCSCVFFKRAVEGQHNILCAGRNDCTIDKIRKNCPCARL 660
Qy 661 QKCLQAGMNLGARKSKKLGLKGIHEBQPOQOQPPPPPPQSPDEGTTYIAPAKESPVN 720
Db 661 QKCLQAGMNLGARKSKKLGLKGIHEBQPOQOQPPPPPPQSPDEGTTYIAPAKESPVN 720
Qy 721 TALVPOLSTISRALTSPVAVLENIPEPIYAGYDSSKPDTAENLSTLNRLAKQMIQ 780
Db 721 TALVPOLSTISRALTSPVAVLENIPEPIYAGYDSSKPDTAENLSTLNRLAKQMIQ 780
Qy 781 VKMAKVLPGFKNPLLEQOITLIQSWMCLSSFALSMRSYKHTNSQPLFYAPDLVFN 837
Db 781 VKMAKVLPGFKNPLLEQOITLIQSWMCLSSFALSMRSYKHTNSQPLFYAPDLVFN 837

RESULT 2
A41401
mineralocorticoid receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 03-Apr-1992 #sequence_revision 03-Apr-1992 #text_change 20-Sep-1999
C:Accession: A41401
R:Patel, P.D.; Sherman, T.G.; Goldman, D.J.; Watson, S.J.
Mol. Endocrinol. 3, 1877-1885, 1989
A:Title: Molecular cloning of a mineralocorticoid (type I) receptor complementary DNA fr
A:Reference number: A41401; MUID:90114194
A:Accession: A41401
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-981 <PAT>
A:Cross-references: GB:M36074; NID:9205340; PID:AAA1583.1; PID:9205341
C:Superfamily: unassigned erba-related proteins; erba transforming protein homology
C:Keywords: DNA binding; transcription regulation; zinc finger
F:602-877/Domain: erba transforming protein homology <ERBA>
F:604-624/Region: zinc finger
F:640-664/Region: zinc finger

Query Match 88.6%; Score 3919.5; DB 2; Length 981;
Best Local Similarity 89.0%; Pred. No. 2/196;
Matches 746; Conservative 35; Mismatches 52; Indels 5; Gaps 2;
```

```
Qy 181 VKSPIMCHEKSPVSCPELNMNTSVCSYPAGINSYSTTASFSGSPVHSPITQGTPLTCSPN 240
Db 181 VKSPITCHEKSSSVSPPLNMASSVCSYPVGINSMSSSTTSRGSFVHSPITQGTSLTCSPS 240
Qy 241 AENRGSRSHSPAHASNVSPLSSPLSSMKSSISSPESHCVKSPVSPNNVTLRSSVSP 300
Db 241 VENRGSRSHSPTHASNVSPLSSPLSSMKSPISSPESHCVKSPVSPNNVTLRSSVSP 300
Qy 301 ANINNSRCVSSPS - NNNNRSTLSSPAASIVGSIQSPVNNAFSTYAGTSAGSSTLRDUV 359
Db 301 ANINNSRCVSSPENNNTNNRSTLSSPAASIVGSIQSPVNNAFSTYAGTSAGSSTLRDUV 360
Qy 360 SPPTQEGAEQVEPPTKEEVEBSAISNGVTGOLNIYOYIKPEPDCAFSSCLGSKINS 419
Db 361 SPPTLHEKGAHDVPPPTKEEVEKAIISNGVTGOLNIYOYIKSEPDGARSSTCLGSKINSISP 420
Qy 420 DQSFQHLSSFPVNTLVESKSHGDLSSRSDGYPLEYIPENYSSSTLRVSSTGSSSRP 479
Db 421 SSFSPVPIKQESTKSCSGTSFKGNPTVNPFPFMDGSYFSFMDKDYYSLSGILGPVPG 480
Qy 480 FDGCEGSGFPVGIKQEPDDGSYPEASIPSSAIVGNSGSGSFHYRIGAOGTISLSRSA 539
Db 481 FDGCEGSAFAFVGIKQEPDDGSYPEASIPSSAIVGNSGSGSFHYRIGAOGTISLSRSP 540
Qy 540 RDQSFQHLSSFPVNTLVESKSHGDLSSRSDGYPLEYIPENYSSSTLRVSSTGSSSRP 599
Db 541 RDQSFQHLSSFPVNTLVESKSHGDLSSRSDGYPLEYIPENYSSSTLRVSSTGSSSRP 600
Qy 600 SKICLVGDEASGCHYGAVTGCSCVFFKRAVEGQHNILCAGRNDCTIDKIRKNCPCAR 659
Db 601 SKICLVGDEASGCHYGAVTGCSCVFFKRAVEGQHNILCAGRNDCTIDKIRKNCPCAR 660
Qy 660 LQKCLQAGMNLGARKSKKLGLKGIHEBQPOQOQPPPPPPQSPDEGTTYIAPAKESPV 719
Db 661 LQKCLQAGMNLGARKSKKLGLKGIHEBQPOQOQPPPPPPQSPDEGTTYIAPAKESPV 716
Qy 720 NTALVPOLSTISRALTSPVAVLENIPEPIYAGYDSSKPDTAENLSTLNRLAKQMIQ 779
Db 717 NSALVPOLSTISRALTSPVAVLENIPEPIYAGYDSSKPDTAENLSTLNRLAKQMIQ 776
Qy 780 VKMAKVLPGFKNPLLEQOITLIQSWMCLSSFALSMRSYKHTNSQPLFYAPDLVFN 837
Db 777 VKMAKVLPGFKNPLLEQOITLIQSWMCLSSFALSMRSYKHTNSQPLFYAPDLVFN 834

RESULT 3
A54273
glucocorticoid receptor - guinea pig
C:Species: Cavia porcellus (guinea pig)
C>Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 23-May-1997
C:Accession: A54273
R:Keightley, M.C.; Fuller, P.J.
Mol. Endocrinol. 8, 431-439, 1994
A:Title: Unique sequences in the guinea pig glucocorticoid receptor induce constituti
A:Reference number: A54273; MUID:94329100
A:Accession: A54273
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-771 <KEI>
A:Cross-references: GB:L13196
C:Superfamily: glucocorticoid receptor; erba transforming protein homology
C:Keywords: zinc finger
F:414-668/Domain: erba transforming protein homology <ERBA>
F:416-436/Region: zinc finger
F:452-476/Region: zinc finger

Query Match 19.6%; Score 865; DB 2; Length 771;
Best Local Similarity 37.4%; Pred. No. 1/3e-37;
Matches 231; Conservative 79; Mismatches 183; Indels 124; Gaps 25;
```



Db 97 MGNDLGF-----QGGQISLPSGETDRLLEESIAN--LRSRTSVENPNKNSAAVSGTPE 151

QY 316 -----TNNRSTLSSPAASTVSGSPVNNAPSYTAAGTSAGSSTLRDVPSPDTQE 366

Db 152 EEPKTDSDLSRPOQMLKSOAGTNGCNVFRPPD-----QSTFDILKLEFFSSGSP 201

QY 367 KGAQGVPE-PKTEEFESAISNVTQOLNIYQIKREPDGAFSSSCLGNSKTNSD-SSFS 424

Db 202 KERSSEPMRPDILLMDESCLLSPAGE-----DDPF--LLEGNS--NECCKPLI 245

QY 425 VPIKESTKHSQSGTSFGKGNPTVNPFPMDGSGYFSFMDKDYLSGLIGPVPFGDNC 484

Db 246 LPDTRPKTKNDNDGLSSNSNV--PQPYK-----MEKEDPIELC-----TPGV----- 287

QY 485 EGSGFPGVIGKQEPDDGSGYYPENASIPSSAIVG-----VNSGGOSFHYRIGAOGTI 533

Db 288 -----IKQE-KLGPIYCAQAFSGANIKMKMSAIVHGVSSTGGQVHYDM--NTA 335

QY 534 SLTSRARQGSFQHLSSFPVNTLVESW-----KSHGDLSSRRSDGYPVLETIPEVWSSST 588

Db 336 SLSSQ-ODQK-PFVNPVPIPVGSENNMRNCGSGEDNLTSLGTVPNPGRSVFSNGYSASP 393

QY 589 LR-----SVTSSSRPKICLVCGDEASGCHGVYTCGCKYEFKRAVGGQNTYCA 640

Db 394 LRPDVSPSPSSSTTTGTPPKICLVCSDEASGCHGVLTGCKYEFKRAVGGQNTYCA 453

QY 641 GRNDCTIDKIRKRNCPACRLQCLQAGNMLGARKSKLGLKGIHEEDPQOQOQPPPPPP 700

Db 454 GRNDCTIDKIRKRNCPACRYRKCQLQAGNMLEARKTKK--KIKGI----- 495

QY 701 POSPEGTTIYAPAKEPSVNTALVPQLSTISKALTPSPVWVLENIPEPLVAGYSSKPD 760

Db 496 ----QAATGVSONTSENNPKTIV--ATLPQ-LRPLTVSLTEVIEPEVHSGYSTSPD 548

QY 761 TAENLSTLTNLRAGKQMIQVYKMAKVLPGFKNLPLEDDITLIQVSMWCSSPALSMRSYK 820

Db 549 STWRIMTITLNLMGQGVIAAYKMAKAIPGFKNLHDDQMTLQIYSWMLMAPALGWRSTK 608

QY 821 HTNSQFLYFADPLVENE 837

Db 609 QNSGSLCFAPDLLINE 625

RESULT 4

S44047

glucocorticoid receptor - African clawed frog

C:Species: *Xenopus laevis* (African clawed frog)

C:Date: 13-Jan-1995 #sequence\_revision 27-Oct-1995 #text\_change 22-Jun-1999

C:Accession: S45348; S44047; S42083

R:Gao, X.; Kalkhoven, E.; Peterson-Maduro, J.; van der Burg, B.; Destree, O.H.J.

A:Title: Expression of the glucocorticoid receptor gene is regulated during early embryonic development

A:Reference number: S45348; MUID:94289478

A:Accession: S45348

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-776 <GAO>

A:Cross-references: EMBL:X72211

A:Experimental source: embryonic stage 17

R:Gao, X.; Kalkhoven, E.; Peterson-Maduro, J.; van der Burg, B.; Destree, O.H.J.

submitted to the EMBL Data Library, May 1993

A:Description: The expression of glucocorticoid receptor gene is regulated during early embryonic development

A:Reference number: S44047

A:Accession: S44047

A:Molecule type: mRNA

A:Residues: 1-271 'R', 273-776 <GAW>

A:Cross-references: EMBL:X72211; NID:9444042; PIDN:CAAS1010.1; PID:9444043

A:Experimental source: embryonic stage 17

R:Picard, D.

submitted to the EMBL Data Library, February 1994

A:Reference number: S42083

A:Accession: S42083

A:Molecule type: mRNA

Query Match	19.4%	Score 856.5	DB 1	Length 776
Best Local Similarity	30.7%	Pred. No. 3.7e-37		
Matches 256	Conservative 90	Mismatches 214	Indels 273	Gaps 29
<p>A:Residues: 452-501, 'P', 503, 'A', 505, 'A', 507-510, 'N', 512-518, 'M', 520-543, 'F', 545-550, A:Cross-references: EMBL:X77764; NID:q456373; PIDD:CAAS4804.1; PID:q456374  A:Experimental source: liver  C:Superfamily: glucocorticoid receptor; erba transforming protein homology  C:Keywords: DNA binding; nucleus; steroid hormone receptor; transcription regulation  F:418-673/Domain: erba transforming protein homology &lt;ERBA&gt;  F:420-440/Region: zinc finger CCCC motif  F:456-480/Region: zinc finger CCCC motif</p>				
QY	41	NYMEIVNVCVGAIPNNSTGGSKKEQELPCLLODNNRPGLIDITKTELESKELSAT	100	
DB	35	NRGCVASV-VASQPTSTASQSNTRQQD---HFKQLATDSDTNGLNANNVPOPLDLSKA	90	
QY	101	VAESKGLV---DSVRADYIYEQDNOOGSKSPAKIYONVQLYKFGKNGHRPSTLSC	156	
DB	91	VLSMGLVYGESDITVYMSSDIAFPQEOIGISTGETDLSLEE-----	133	
QY	157	VATPLRSEMSDSSVNGVMRAIYKSPIMCEKSPSVCSPLNMTNMSVCPAGINSYST	216	
DB	134	-----SINLQAKSLAPKLEISD	154	
QY	217	TASFQSPVHSPITTOGTPLTCSMAENRGRSHSPAHASNVSPSSPLSSKSSISSPP	276	
DB	155	PGGF-----KCDISAQPRPSMOGGSGNS-----SINLFPK	186	
QY	277	SHC-----SYKSPVSPNNVTLNRSSVSPANINNSRCVSSPSNTNRSSTLSSPA	326	
DB	187	DOCTDRLRLDLGISDPSIDPKGSNPWL-----DPLFDEQEAENLLSPLOT-----	231	
QY	327	ASTVSGISPVNNAASYTASGTSAGSSTLRDVPSPDQEKGAQVPPPKTEVEVSATSN	386	
DB	232	-----GDPPFMSEVLSBGSKTL-----SLEDGTQR-----	257	
QY	387	GVTGQNLIVQYIKPPDGAFFSSSCGSGNSKINSDSFVPIRQESTKHKSGSTSEKGNPT	446	
DB	258	-----LGDHAKMDLLRSADPPISQVYT-----	279	
QY	447	VNPPPMDSGYSPFMDKDYSL--SGILGRPVG---FDGNCESGSPFVGIKQEPDGS	501	
DB	280	-----EKEDYIELCTPGVYNEKFGPPVYCNGFSGSGL-FGNK-----	316	
QY	502	YYPEASIPSSAIV--GVN-SGGSQFHYRIGAGCTISLSASANDQFOHLSSFPNTLVE	558	
DB	317	-----SSAITSVHGVSISGGOMHYDL--NTATISQDDYKPVF-NLGS--PQTSIAE	362	
QY	559	SW-KSHGD---LSSRRSDGYPVLEYIPENVSSSTLRS-----VSTGSSRPKICLV	605	
DB	363	GMNRCHGSGNDPAAPRGVNNFPNRSVFSNGYSPPGIRSDASPSSTSTGTPPKCLLV	422	
QY	606	CGDEASGCHYGVNTGSGCKVFFKRAVEGSOHNYLACGRNDCTIDKIRKNCPACRYLOKLO	665	
DB	423	CGDEASGCHYGVNTGSGCKVFFKRAVEGSOHNYLACGRNDCTIDKIRKNCPACRYRKCLO	482	
QY	666	AGMNLGARKSKKLGLKLGHEBQPOQOQPPPPPPPOSEBEETIYA-PAKPSYNTALY	724	
DB	483	AGMNLGARKTKK-KIKGI-----QOSTTATARSPESTSMTRLV	520	
QY	725	PLQSTIRSLRPLSPVAVLENIEPIYAGYDSKPDTEFNILSTNIRLAGKOMIYVMA	784	
DB	521	P--ASVAQ-LPFTLLISLLEVEPLVLYGYSDSIDPTTIRLMSSINMLGKRGVAVSAVMA	577	
QY	785	KVLPGFKNLPLEDQITLLIOYSMMCLSSPALSRSRYKHTNSQFLYEPAPLVENE	837	
DB	578	KALPGFRNLHDDQMTLLQYSMFLMVFALGKRYSKQINGSLIYAPPLVITE	630	

glucocorticoid receptor, beta splice form human  
N:Alternate names: hgr  
C:Species: Homo sapiens (mam)  
C:Date: 04-Dec-1986 #sequence\_revision 04-Dec-1986 #text\_change 21-Jul-2000  
C:Accession: B93370; B39779; A03247  
R:Hollenberg, S.M.; Weinberger, C.; Ong, E.S.; Cerelli, G.; Oro, A.; Lebo, R.; Thompson, Nature 318, 653-661, 1985  
A:Title: Primary structure and expression of a functional human glucocorticoid receptor  
A:Reference number: A93370; MUID:B6092206  
A:Accession: B93370  
A:Molecule type: mRNA  
A:Residues: 1-742 <HOL>  
A:Cross-references: EMBL:X03346; GB:M11050; MIM:q31681; PIDN:CA27054.1; PID:q31682  
R:Enclio, I.J.; Detera-Wadleigh, S.D.  
J. Biol. Chem. 266, 7182-7188, 1991  
A:Title: The genomic structure of the human glucocorticoid receptor.  
A:Reference number: A39779; MUID:91201378  
A:Accession: B39779  
A:Status: nucleic acid sequence not shown; not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 385-404; 441-459; 480-498; 573-593; 621-640; 665-685; 718-737 <ENCC>  
A:Cross-references: GB:M60597  
A:Experimental source: Placenta  
R:Weinberger, C.; Hollenberg, S.M.; Rosenfeld, M.G.; Evans, R.M.  
Nature 318, 670-672, 1985  
A:Title: Domain structure of human glucocorticoid receptor and its relationship to the v  
A:Reference number: A93373; MUID:B6092211  
A:Contents: annotation; domains  
C:Comment: Alpha (see PIR:QH00A) and beta splice forms differ in their carboxyl-termina  
however, it is possible that variant receptors perform tissue-specific functions.  
C:Genetics:  
A:Gene: GDB:GRL  
A:Cross-references: GDB:120017; OMIM:138040  
A:Map position: 5q31-5q31  
A:Introns: 395/2; 451/1; 490/1; 583/1; 631/2; 675/1; 727/3  
A>Note: the first intron occurs before the initiator codon  
C:Superfamily: glucocorticoid receptor; erba transforming protein homology  
C:Keywords: alternative splicing; DNA binding; nucleus; steroid hormone receptor; transcr  
?413-674/Domain: erba transforming protein homology <ERBA>  
?421-441/Region: zinc finger CCCC motif  
?457-481/Region: zinc finger CCCC motif

```

Query Match          19.4%; Score 856; DB 1; Length 742;
Best Local Similarity 35.0%; Pred. No. 3.7e-37;
Matches 239; Conservative 83; Mismatches 212; Indels 148; Gaps 25.

OY      248 SHSPAHASVGVGSLPSLSSMKSSISSPPSHCSYKSPSSPNNTLRRSSSPANNNNSR 307
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      6 SLTPRENPSSVTLQERGDVMPFKTLRGATVAVXSASP-----LVAASQSDSKOR 60
OY      308 CSVSSPSMNTNNS-----TLSSPAASTVGV-----SICSPVNNARSYTASG---TSAGSSTR 356
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      61 LLVDPPKGSVSAQAQPDLSKAVSLAMGLMGTETKRYMGNDLGFQOQOGLSSSGETDLK 120
OY      357 DVVPS-----PDRQEKGAQ-----EVPPKTEEVESAISNGVTQOLINVOYI 398
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      121 LLEESIANLNKSTVSPENDKSSATSAVASAPAEKEFEKPTHSDVSSBOQLKQO----- 173
OY      399 KEPPGAPSSSCLGNSKI--NSDSFSV-----PIQESTKHSCSGTSKRGNT 446
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      174 -----TGINGNVKLYTTDSTFDLQDLERSSGSPGKETESPWRSDLLIDENCL 224
OY      447 VNPFFMDSGYF-----SFMDKDYV--SLSGILGPPVPGFDNC 485
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      225 LSPLAGEDDSFLLEGNSNEDCKPLLIPTRKPIKNDGLVLSSPSKAVTLPQY----KTE 279
OY      486 GSGF-----PVGIKQEPDDGSYYPEASIPSSAIVG-----VNSGGQSFHYRIGA 529
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      280 KEDFIELCTPGVTKQD-KIGTYVCCASFPFGANITGNKMAISVHGAVSTSGGOMYTHDM-- 336
OY      530 QGTISLSRARDQSFQHLSSFPVNTLVESW---KSHGD--LSRRSDGYPVLEYIIPENV 584
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

[illegible]

RESULT 6

QNHUSA

glucocorticoid receptor, alpha splice form - human

N:Alternate names: hGR

C:Species: Homo sapiens (man)

C:Date: 04-Dec-1986 #sequence revision 04-Dec-1986 #text change 21-Jul-2000

C:Accession: A93370; A39837; A39779; I56596; A03246; A32156

R:Hollenberg, S.M.; Weinberger, C.; Ong, E.S.; Cerelli, G.; Oro, A.; Lebo, R.; Thompson

Nature 318, 635-641, 1985

A:Title: Primary structure and expression of a functional human glucocorticoid receptor

A:Reference number: A93370; MUID:86092206

A:Accession: A93370

A:Molecule type: mRNA

A:Residues: 1-777 <HOL>

A:Cross-references: EMBL:X03225; GB:M10901; NID:g31679; PIDN:CAA26976.1; PID:g31680

R:Leclercq, S.; Xie, B.; Roy, R.; Govindan, M.V.

J. Biol. Chem. 266, 8711-8719, 1991

A:Title: Purification of a human glucocorticoid receptor gene promoter-binding protein

A:Reference number: A39837; MUID:91224961

A:Accession: A39837

A:Molecule type: DNA

A:Residues: 1-394 <LEC>

A:Cross-references: GB:M69104; NID:g183605; PIDN:AAA8049.1; PID:g553322

R:Enco, I.J.; DeTea-Wadleigh, S.D.

J. Biol. Chem. 266, 7182-7188, 1991

A:Title: The genomic structure of the human glucocorticoid receptor.

A:Reference number: A39779; MUID:91201378

A:Accession: A39779

A>Status: nucleic acid sequence not shown; not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 385-404; 441-459; 480-498; 573-593; 621-640; 665-685; 718-737 <ENC>

A:Cross-references: GB:M60597

A:Experimental source: Placenta

R:Weinberger, C.; Hollenberg, S.M.; Rosenfeld, M.G.; Evans, R.M.

Nature 318, 670-672, 1985

A:Title: Domain structure of human glucocorticoid receptor and its relationship to the

A:Reference number: A93373; MUID:86092211

A:Contents: annotation; domains

R:Dahlman, K.; Stromstedt, P.E.; Rae, G.; Joernvall, H.; Flock, J.I.; Carlstedt-Duke

J. Biol. Chem. 264, 804-809, 1989

A:Title: High level expression in *Escherichia coli* of the DNA-binding domain of the g

A:Reference number: A32156; MUID:85093147

A:Contents: annotation; domains

A>Note: engineered sequence expressed in *Escherichia coli*

R:Govindan, M.V.; Pothier, F.; Leclercq, S.; Palaniswami, R.; Xie, B.

J. Steroid Biochem. Mol. Biol. 40, 317-323, 1991

A:Title: Human glucocorticoid receptor gene promoter-homologous down regulation.

A:Reference number: I56596; MUID:92068829

A:Accession: I56596

A>Status: preliminary; translated from GB/EMBL/DBJ



Db 189 QNRKST-----GTMGSGKLYPTDOSTFDLKL-DLEFSAGSPSKDNTNSPMKRDLLIDE 242  
QY 302 NNNNSRCVSYSP-----SNTNNRSTLSSPAASTVGSICSPVNNAFSYTASGTSAGSSTLRD 357  
Db 243 NLLSLPLAGDDPFLLEGNINED-----CKP----- 267  
QY 358 VVPSPTQKGAQAEVFPFPTVEESAIISNGVIGOLNIYQYIKPEPDGAFSSSCGLGNSKI 417  
Db 268 -LILPDTK-----PKIKDT-----GDTIL 285  
QY 418 NSDSFSV-IKQESTKHSCSGTSFGKGNPTVNPFPMDGSYFSFMDKDYLSGLILGP 476  
Db 286 SSPSSVALQVETK-----DFITELC----- 307  
QY 477 VPEFGDNCESGSGFPVIGIKQEPDDGYPEASIPSSAIVG-----VNSGGSFHY 525  
Db 308 TPGV-----IKQE-KLGPYCOASFSGTNIIGNKMSAISVHGVSSTSGOMYHY 354  
QY 526 RICAQGTILSRARQSGFOHLSFPFVNTLVESMK-----SHGDL-----SRR 570  
Db 355 DM--NTASLSQO-QDQK-PVEFNVPPIPVGSENNMRGCGSGEDSLTSLGALMFGERSVF 409  
QY 571 SDGYPVLEYIPENVSSSTLRSVSTGSSRPSKICLVCGDEASGCHGVNTGSCVYFKKRA 630  
Db 410 SNGYSSPGMRPDVSSPPSSSAATGP--PPKICLVCSDEASGCHGVLTGSCCKVYFKRA 467  
QY 631 VEGOHNYLACGRNDCTIDKIRKNCAPACRLQKCLQAGMNLGAKSKKLKIGIHEDQ 690  
Db 468 VEGOHNYLACGRNDCTIDKIRKNCAPACRYRCKLQAGMNLGAKSKKLKIGIHEDQ 525  
QY 691 QQGPPEPPPEPQSEGTITYIAPAKEPSVNTALVPQLSTISRALTSPVWLENIEPEIV 750  
Db 526 VSG-----DISENPNTIYPAALPQ-----LPTLVLSLEVEIEPEVL 562  
QY 751 YAGYDSSKPDPTAENLSTLNLRLAGKOMIOYVKAAYLPGFKNLPLEDQITLIDYSMWCLIS 810  
Db 563 YAGYDSSVPPSARIMRTITLMLGROVIAVKAWAKAILGRNLHLDQMTLLQYSWMFLM 622  
QY 811 SFALSWRSYKHTNSQFLYFAPDLVNE 837  
Db 623 AFALGWRSTYRQSSGNLTCFAPDLLINE 649  
RESULT 8  
A25691  
glucocorticoid receptor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 05-Jun-1988 #sequence\_revision 18-Nov-1994 #text\_change 22-Jun-1999  
C:Accession: A25691; S02212; S02214  
R:Danielson, M.; Northrop, J.P.; Ringold, G.M.  
EMBO J. 5, 2513-2522, 1986  
A>Title: The mouse glucocorticoid receptor: mapping of functional domains by cloning, se  
A:Reference number: A25691; M0ID:87053816  
A:Accession: A25691  
A:Molecule type: mRNA  
A:Residues: 1-783 <DAN>  
A:Cross-references: GB:X04435; NID:951057; PIDN:CAA28031.1; PID:951058  
R:NoHo, T.; Kasai, Y.; Saito, T.  
Nucleic Acids Res. 17, 445, 1989  
A>Title: Novel cDNA sequence possibly generated by alternative splicing of a mouse glucoc  
A:Reference number: S02212; M0ID:89098404  
A:Accession: S02212  
A:Molecule type: mRNA  
A:Residues: 1-436, 'G', '438-755 <NOH>  
A:Cross-references: EMBL:X13358; NID:951117; PIDN:CAA31738.1; PID:951118  
A:Note: neither the complete nucleic acid sequence nor the complete translation are show  
A:Accession: S02214  
A:Molecule type: mRNA  
A:Residues: 1-436, 'G', '438-458, 'R', '459-755 <NO2>  
A:Cross-references: EMBL:X13359; NID:951119; PIDN:CAA31739.1; PID:951120  
A:Note: neither the complete nucleic acid sequence nor the complete translation are show  
C:Superfamily: glucocorticoid receptor; erba transforming protein homology

C:Keywords: alternative splicing; DNA binding; nucleus; steroid hormone receptor; tra  
F:75-82/Region: glutamine-rich  
F:426-680/Domain: erba transforming protein homology <ERBA>  
F:428-448/Region: zinc finger CCCC motif  
F:464-488/Region: zinc finger CCCC motif  
F:734-783/Domain: steroid binding #status predicted <STR>

Query Match 19.0%; Score 842; DB 1; Length 783;  
Best Local Similarity 30.6%; Pred. No. 2.1e-36;  
Matches 261; Conservative 80; Mismatches 197; Indels 314; Gaps 30;

QY 46 VNVSCVSGAIPNNSTOGSSKEKQELLPC-----LQDNNRPGILYSDIKTELESKE 96  
Db 40 VAVSASPSVA--AAQADSKQORILLDFSGSASNAQ00000QDP-----QPD 86  
QY 97 LSATVAESKGLYM---DSVRADYSTEQDQNGSMSPRAKIYQNYEQLYKTKGNGHPS 152  
Db 87 LSKAVLSMGLYMETETKVMGNDLGYPQOQGLISGETDRLLEE----- 133  
QY 153 TLSCVNTPLRSPMDSGSSVNGVMRAIYKSPIMCHEKSPVCSPLNMTSYCSFAGINS 212  
Db 134 -----STANLNRSRPRE--NP 148  
QY 213 VSTTASFGSPFVHSPITQGTPLTCSPAENRGRSHSPAHASNVGSPLSPLSMKST 272  
Db 149 KSTPA-----GCATPEKEFPQTHSP-----SSEQNRKS-- 181  
QY 273 SSPSHCSKSVSSPNNTLRSVSSPANI--NSRCSVSSPNTNNRS-----T 321  
Db 182 -----QGTNGSGKLYTTDOSTFDLQDLFEASGSGKETNESPMKRDLLIDEN 231  
QY 322 LSSPA-----STVSGISPVNNAFSTASGTSAGSTLTDVPSPTQKGAQEV 372  
Db 232 LSLPLAGEDPFLLEDGVNEDCKP-----LILPDTK----- 262  
QY 373 PPPKTEVSAISNGVTGOLNIYQYIKPEPDGAFSSSCGLGNSKINSOSSEVF--IKQES 431  
Db 263 --PKTODT-----GDTILSSPSVALPVQVETK 288  
QY 432 TRHSCGTSFKGNPTVNPFPMDGSYFSFMDKDYLSGLIGPPVPGFDGNCESGSPV 491  
Db 289 -----DPFIELC-----TPGV----- 299  
QY 492 GIKQEPDDGYPEASIPSSAIVG-----VNSGGSFHYRILGAQGTISLRAR 540  
Db 300 -IKQE-KLGPYCOASFSGTNIIGNKMSAISVHGVSSTSGOMYHYDM--NTASLSQO-Q 353  
QY 541 DQSFQHLSEFPVNTLVESMK-----SHGDL-----SRSDGYPVEIYIPENVS 585  
Db 354 DQK-PVEFNVPPIPVGSENNMRGCGSGEDNLTSLGAMNAGRSVFSNGTSFGMRPD--V 410  
QY 586 SSTLRSVSTGSSRPSKICLVCGDEASGCHGVNTGSCVYFKKRAVEGQHNLYACGRND 645  
Db 411 SSPSSSSTATGPPPKLCLVCSDEASVCHGYVLTGSCCKVYFKRAVEGQHNLYACGRND 470  
QY 646 IIDKIRKNCAPACRLQKCLQAGMNLGAKSKKLKIGIHEDQPOQOQPPPPPPQSE 705  
Db 471 IIDKIRKNCAPACRYRCKLQAGMNLGAKSKKLKIGIHEDQTAGVSO-----DTSE 520  
QY 706 EGTITYIAPAKEPSVNTALVPQLSTISRALTSPVWLENIEPEIVYAGDSSKPDPTAENL 765  
Db 521 NANKTIVPALPQ-----LPTLVLSLEVEIEPEVLVYAGDSSVPSASAMR 565  
QY 766 LSTLNLRLAGKOMIOYVKAAYLPGFKNLPLEDQITLIDYSMWCLISFALSWRSYKHTNSQ 825  
Db 566 MTLNLNLGROVIAVKAWAKAIPGFRNLHLDQMTLLQYSWMFLMFAFGWRSYRQASGN 625  
QY 826 ELYFAPDLVNE 837  
Db 626 LILCFAPDLLINE 637



[illegible]

A:Cross-references: CB:M37518  
R:Conneely, O.M.; Sullivan, W.P.; Toft, D.O.; Birnbaumer, M.; Cook, R.G.; Maxwell, B.  
Science 233, 767-770, 1986  
A>Title: Molecular cloning of the chicken progesterone receptor.  
A:Reference number: A24661; MUID:86289413  
A:Accession: A24661  
A:Molecule type: mRNA  
A:Residues: 128-133, 'E', 135-147, 'E', 149-164 <C02>  
A>Note: The authors translated the codon CAG for residue 7 as Glu and CAG for residue  
R:Jeltsch, J.M.; Krozowski, Z.; Quirin-Sticker, C.; Gronemeyer, H.; Simpson, R.J.; G.  
Proc. Natl. Acad. Sci. U.S.A. 83, 5424-5428, 1986  
A>Title: Cloning of the chicken progesterone receptor.  
A:Reference number: A24312; MUID:86287271  
A:Accession: A24312  
A:Molecule type: mRNA  
A:Residues: 417-490 <E2>  
A:Cross-references: GB:M14280; NID:g212607; PIDN:AAA4903.1; PID:g212608  
A>Note: amino acid and corresponding nucleotide sequences are also shown for three sm  
R:Birnbaumer, M.; Himrichs-Bosello, M.V.; Cook, R.G.; Schrader, W.T.; O'Malley, W.  
Mol. Endocrinol. 1, 249-259, 1987  
A>Title: Chemical and antigenic properties of pure 108,000 molecular weight chick pro  
A:Reference number: A40911; MUID:88288199  
A:Accession: A40911  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 128-133, 'E', 135-147, 'E', 149-164, 546-558 <BIR>  
R:Simpson, R.J.; Grego, B.; Govindan, M.V.; Gronemeyer, H.  
Mol. Cell. Endocrinol. 52, 177-184, 1987  
A>Title: Peptide sequencing of the chick oviduct progesterone receptor form B.  
A:Reference number: A61552; MUID:88005426  
A:Accession: A61552  
A:Molecule type: Protein  
A:Residues: 136-153; 168-174; 195-228; 526-537, 'X', 539; 546-563 <SIM>  
C:Genetics:  
A:Introns: 400/2; 451/1; 490/1; 591/1; 639/2; 683/1; 735/3  
C:Superfamily: progesterone receptor; erba transforming protein homology  
C:Keywords: DNA binding; nucleus; steroid hormone receptor; zinc finger  
P:1-786/Product: progesterone receptor form B #status predicted <MA>  
F:128-786/Product: progesterone receptor form A #status predicted <MA2>  
F:419-682/Domain: erba transforming protein homology <ERBA>  
F:421-441/Region: zinc finger  
F:457-481/Region: zinc finger

```

Db      484 AGMVLGGRKFKLNNKMKVFTLIDVALQOPAVLIDBETSLQTRLSP-SPNGE-----IP 535
Oy      726 OLSTSRALTFSPVAVLENIPPEIYVAGYDSSKRPDTAENLSTLRLNLAGKQMIQVYKAK 785
Db      536 -----FVPMISIVLGEIPEVYVAGYDNTKPTPSSLLTSLNLHLCEROLLGVYKMSK 587
Oy      786 VLPGRKNIPLDQDTLLIOYSMMCLSSFALMSRKYKHTNSQFLYFAPDLVFNELLARVE 844
Db      588 LLPGFRNIHIDDQTLTLOYSNMSLWVFAMGMRKYKHYVSGQMLYFAPDLILNE-QRMKE 644

RESULT 12
A39596
progesterone receptor B form - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 20-Aug-1999
C:Accession: A39596; I49111
R:Schott, D.R.; Shyamala, G.; Schneider, W.; Parry, G.
Biochemistry 30, 7014-7020, 1991
A:Title: Molecular cloning, sequence analyses, and expression of complementary DNA encod
A:Reference number: A39596; MUID:91299759
A:Accession: A39596
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-923 <SCH>
A:Cross-references: GB:M68915; GB:J05333; NID:q200471; PIDN:AAA39971.1; PID:q200472
R:Hagihara, K.; Wu-Peng, X.S.; Funabashi, T.; Kato, J.; Pfaff, D.W.
Biochem. Biophys. Res. Commun. 205, 1093-1101, 1994
A:Title: Nucleic acid sequence and DNase hypersensitive sites of the 5' region of the m
A:Reference number: I49111; MUID:95100931
A:Accession: I49111
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-9 <HAG>
A:Cross-references: EMBL:U12644; NID:g639916; PIDN:AA66067.1; PID:g639917
C:Superfamily: progesterone receptor; erba transforming protein homology
C:Keywords: DNA binding; nucleus; steroid hormone receptor; transcription regulation; z
F:557-577/Region: zinc finger
F:593-617/Region: zinc finger

Query Match      18.2%; Score 804; DB 2; Length 923;
Best Local Similarity 30.3%; Pred. No. 2.5e-34;
Matches 251; Conservative 94; Mismatches 249; Indels 234; Gaps 33;

Oy      181 VKSPIMCH-EKSPVSCPLNMTSSVCSGAGIN-----SVSS 215
Db      24 IGSPLARLDGSPGOGSOHSDSVSVSPISLQGLFPSCRCGPDLDPGKTGDQSLSD 83
Oy      216 TTASGFSEFVPSHPTQGTPLTCSFPAENRGSRSHSPAHSN--VGSPLSLPL--SSMKS 271
Db      84 VEGAF-----SGVEAT-----HREGGRNSRPPEKSDRLDLSDVLDLSLTLPBGPPQS 128
Oy      272 ISSPPSHCSVKS-----PVSSPNNVTLRSSVSSPANINNSRCSVSSPNTNNRSTLS 323
Db      129 HASPPACAIITSMCLFGPELP-EDPRSVPATKGLSLPL-MSRPEIKVGDQSGTGQGVK 186
Oy      324 SPASSTVOSICSPVNNASTYASGTSAGSSTLRDVPSPDPDQEKAGQVFPKTEVESA 383
Db      187 PKGLSPPRQLLPLPFGSNAHPCAG-----VKPSPO-----PAAGEVEE- 224
Oy      384 ISNGVTGQLNIYQYIKPEPDGAFSSSLCGNSKINS-----DSSFSVP--- 426
Db      225 -DSGLEMGSGASPLLKSRP-RALEGTGGGGVAAANAPAAAGCVTLVYKEDSRFSAPRYS 282
Oy      427 IKQES-----TKHSCSGTSEFGNPTVNPF----- 450
Db      283 LEQDPIAPGRSLPATTYVDFIHWPIPLNHALLAARTROLLEGESYDGAGATAGFCPR 342
Oy      451 -----PMDGYSYFSFMDDK-DYISLSG-----ILGPPVPG 479

```

Db 343 SPSPAPFPVPVGPDPDCTYPLEGDPKEDVFPFLYGDFOPTGKLIKEEEGADAAVRSPRY 402

QY 480 FDGCEGS---GFVGVGIKQEPDGSITYPEASI---PSSAIVG-VNSGGQSFH---YATGA 529

Db 403 LSAQASSSTPPDFPLAPAPQAAPSSRPGEEAAVAGPSSAAVSPASSSGSALECLILYKAA 462

QY 530 QGTISLSASANDQSFQHLSSFP-----VNTLVESW 560

Db 463 PPT-----QGSFAPLPCKPPAAASCLLPDLSLPAAPGTAAPAYIQLGLGLPOLG 514

QY 561 KSHDLSRRSDGY-PVLEYI-PENVSSSTLRVSTG-SRPSKICLVCGDEASGCHYV 617

Db 515 YQAAVLKDSLPQVPPPLTYLNTLRPDEAS--QSPQYGFDSLPQKICILICGDEASGCHYV 571

QY 618 VTGSGCKVEFFKRAVEGQHNTLCAGRNDICIIRKKNCPACRICKCLQAGNMLGARKSK 677

Db 572 LTGSCSKVEFFRAMEGQHNTLCAGRNDICIYDKIRKKNCPACRICKCCQAGVNLGSRKFK 631

QY 678 LGLKLGIE-EQPOQOQPPPPPPQSPBEETTYIAAKERSVNTALVPQLSTISRALTP 736

Db 632 FNKRVMTLTLGVALPQSVGLPNESQALSORITP-----SPNOEIOVPLP----- 677

QY 737 SPVAVLEINPEIPEIYAGYDSSKPTAENLSTLRKLGKQIOYVAKAVLPGEKNTPLE 796

Db 678 --INLMSIEDVITYAGHDNKTPTSSSLTSLMQLGEBROLISVYKSKSLPGFRNLHID 735

QY 797 DQITLIQYSWMCSSFALSWSRYKHTNSQELFAPADLVFNELLARVE 844

Db 736 DQITLIQYSWMSLWVFGIWMRSYKHSQMLYFAPDILNE--QRME 781

RESULT 13

QRHUP

progesterone receptor form B - human

N:Alternate names: hPR

N:Contains: progesterone receptor form A

C:Species: Homo sapiens (man)

C:Date: 30-Jun-1987 #sequence\_revision 18-Nov-1994 #text\_change 22-Jun-1999

C:Accession: S09971; S12464; A03245

R:Kastner, P.; Krust, A.; Turcotte, B.; Stropp, U.; Tora, L.; Gronemeyer, H.; Chambon

EMBO J. 9, 1603-1614, 1990

A:Title: Two distinct estrogen-regulated promoters generate transcripts encoding the

A:Reference number: S09971; MUID:90228361

A:Accession: S09971

A:Molecule type: mRNA

A:Residues: 1-933 <KAS>

A:Cross-references: EMBL:X51730

R:Kastner, P.

Submitted to the EMBL Data Library, February 1990

A:Reference number: S12464

A:Accession: S12464

A:Molecule type: mRNA

A:Residues: 1-343, 'T', 345-933 <KA2>

A:Cross-references: EMBL:X51730; NID:g35651; PIDN:CA36018.1; PID:g35652

R:Mirault, M.; Aegerter, M.; D'Audiot, L.; Loosfelt, H.; Merlie, C.; Fridlansky, F.; Guil

Biochem. Biophys. Res. Commun. 143, 740-748, 1987

A:Title: Complete amino acid sequence of the human progesterone receptor deduced from

A:Reference number: A03245; MUID:87184565

A:Accession: A03245

A:Molecule type: mRNA

A:Residues: 1-225, 'G', 227-255, 'V', 257-659, 'V', 661-933 <M5>

A:Cross-references: GB:M15716; NID:g189934; PIDN:AAA60081.1; PID:g189935

C:Genetics:

A:Gene: GDB:PCR

A:Cross-references: GDB:119493; OMIM:264080

A:Map position: 11q22.1-11q22.3

C:Keywords: progesterone receptor; erba transforming protein homology

C:Keywords: alternative splicing; DNA binding; nucleus; phosphoprotein; steroid hormo

E:1-933/Product: progesterone receptor form B #status predicted <M1>

E:165-933/Product: progesterone receptor form A #status predicted <MA2>

E:565-829/Domain: erba transforming protein homology <ERBA>

F:567-867/Region: zinc finger CCCC motif

F:603-627/Region: zinc finger CCCC motif







Db 685 -----INLMSTLEPDVIVAGHDNTPKDPDTSSLLTSTLNQGEROLLSVYKWSKSLP 734

OY 789 GFKNPLEDDOTTLIOYSMCMSSFALMSRSYKHNISOFLYAPDLYFNEELLARRE 844

Db 735 GFRNLHDDOTTLIOYSWMSLMVFGLGWRSYKHVSGOMLYFAPDPLLINE--QRMKE 788

RESULT 15

A35895

androgen receptor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 31-Oct-1990 #sequence,revision 31-Oct-1990 #text,change 20-Sep-1999

C:Accession: A35895; A37255; A37908; S34398; S17198; S40626; I49501; S12082

R:He, W.W.; Fischer, L.M.; Sun, S.; Bilharitz, D.L.; Zhu, X.; Young, C.Y.F.; Kelley, D.B.

Biochem. Biophys. Res. Commun. 171, 697-704, 1990

A:Title: Molecular cloning of androgen receptors from divergent species with a polymerase

epitor cDNA probes from dog, guinea pig and clawed frog.

A:Reference number: A35895; MUID:90386642

A:Accession: A35895

A:Molecule type: mRNA

A:Residues: 1-899 <HEA>

A:Cross-references: EMBL:X53779; NID:g49966; PIDN:CAA37795.1; PID:g49967

R:Gaspar, M.L.; Meo, T.; Tosi, M.

Mol. Endocrinol. 4, 1600-1610, 1990

A:Title: Structure and size distribution of the androgen receptor mRNA in wild-type and

A:Reference number: A37255; MUID:91133433

A:Accession: A37255

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-899 <GAS>

A:Cross-references: GB:S37890; NID:g191935; PIDN:AAA37234.1; PID:g191936

R:Charest, N.J.; Zhou, Z.; Lubahn, D.B.; Olsen, K.L.; Wilson, E.M.; French, F.S.

Mol. Endocrinol. 5, 573-581, 1991

A:Title: A frameshift mutation destabilizes androgen receptor messenger RNA in the Tfm

A:Reference number: A37908; MUID:92017874

A:Accession: A37908

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-899 <CHA>

A:Cross-references: GB:S56585; NID:g236048; PIDN:AA819916.1; PID:g236049

R:Feber, P.W.; King, A.; van Rooij, H.C.J.; Brinkmann, A.O.; de Both, N.J.; Trapman, J.

Biochem. J. 278, 269-278, 1991

A:Title: The mouse androgen receptor. Functional analysis of the protein and characteriz

A:Reference number: S17198; MUID:91354214

A:Accession: S34398

A:Molecule type: DNA

A:Residues: 1-899 <FAB>

A:Cross-references: EMBL:X59592; NID:g49968; PIDN:CAA42160.1; PID:g49969

A:Accession: S17198

A:Molecule type: mRNA

A:Residues: 1-899 <FA2>

A:Cross-references: GB:S59592; NID:g49968; PIDN:CAA42160.1; PID:g49969

R:He, W.W.; Kumar, M.V.; Tindall, D.J.

Nucleic Acids Res. 19, 2373-2378, 1991

A:Title: A frame-shift mutation in the androgen receptor gene causes complete androgen

A:Reference number: S40626; MUID:91252278

A:Accession: S40626

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 366-413 <HEW>

A:Cross-references: EMBL:X53779

R:Gaspar, M.

Proc. Natl. Acad. Sci. U.S.A. 88, 8606-8610, 1991

A:Title: A single base deletion in the Tfm androgen receptor gene creates a short-lived

A:Reference number: I49501; MUID:92020902

A:Accession: I49501

A:Status: preliminary; translated from GB/EMBL/DBD

A:Molecule type: mRNA

A:Residues: 1-899 <RSS>

A:Cross-references: GB:S37890; NID:g191935; PIDN:AAA37234.1; PID:g191936

C:Genetics:

C:Introns: 518/2: 569/1: 608/1: 704/1: 752/2: 796/1: 848/3

C:Superfamily: unassigned erba-related proteins; erba transforming protein homology

C:Keywords: DNA binding; transcription regulation; zinc finger  
E:1-536/Domain: regulatory #status predicted <RGC>  
E:537-795/Domain: erba transforming protein homology <ERBA>  
F:539-559/Region: zinc finger  
F:575-599/Region: zinc finger  
E:650-899/Domain: hormone binding #status predicted <LHG>

Query Match	17.2%;	Score 760;	DB 2;	Length 899;
Best Local Similarity	29.0%;	Pred. No. 4.7e-32;		
Matches 223;	Conservative 90;	Mismatches 211;	Indels 244;	Gaps 25;

[illegible]

Search completed: September 13, 2002, 10:16:58  
Job time: 62 sec

This Page Blank (uspto)

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 13, 2002, 10:17:01 ; Search time 15.02 Seconds  
(without alignments)  
2178.297 Million cell updates/sec

Title: US-09-695-293-42

Sequence: 1 METKGYHSLPEGLDMERRWG.....FLYFAPDLVFNELLARVRWG 845

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues  
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4385	99.2	984	1	MCR_HUMAN
2	3985.5	90.1	977	1	MCR_TUPGB
3	3919.5	88.6	981	1	MCR_RAT
4	1763.5	39.9	612	1	MCR_XENLA
5	857	19.4	776	1	P49844 xenopus lae
6	856	19.4	777	1	GCR_HUMAN
7	854	19.3	776	1	GCR_TUPGB
8	853	19.3	777	1	GCR_AOTNA
9	853	19.3	777	1	GCR_SAIBB
10	850.5	19.2	771	1	GCR_CAVPO
11	847.5	19.2	703	1	GCR_PIG
12	845	19.1	777	1	GCR_SAGE
13	842	19.0	783	1	GCR_MOUSE
14	841.5	19.0	795	1	GCR_RAT
15	840.5	19.0	778	1	GCR_SAISC
16	823	18.6	923	1	PRGR_RAT
17	814.5	18.4	758	1	PRGR_MOUSE
18	806.5	18.2	807	1	GCR_PAROL
19	806	18.2	933	1	PRGR_HUMAN
20	805	18.2	786	1	PRGR_CHICK
21	804	18.2	923	1	PRGR_MOUSE
22	800	18.1	930	1	PRGR_RABIT
23	769	17.4	907	1	ANDR_CANFA
24	760	17.2	899	1	ANDR_MOUSE
25	759.5	17.2	377	1	PRGR_SHEEP
26	758.5	17.2	902	1	ANDR_RAT
27	751.5	17.0	884	1	ANDR_EULFC
28	738	16.7	895	1	ANDR_PAPHA
29	736	16.6	895	1	ANDR_MAFPA
30	736	16.6	911	1	ANDR_PANTAR
31	731.5	16.5	919	1	ANDR_HUMAN
32	722	16.3	709	1	ANDR_RABIT
33	461.5	10.4	586	1	ESR1_XENLA

34	455.5	10.3	180	1	PRGR_MACEU	P79373 macropus eu
35	455.5	10.3	589	1	ESR1_CHICK	P06212 gallus gall
36	453.5	10.3	587	1	ESR1_POESU	O91250 poephila gu
37	452.5	10.2	595	1	ESR1_MESAU	O94235 mesocricetu
38	452.5	10.2	595	1	ESR1_PIG	O29040 sus scrofa
39	447.5	10.1	594	1	ESR1_HORSE	O91V98 equus caball
40	445.5	10.1	595	1	ESR1_HUMAN	P03372 homo sapien
41	440.5	10.0	599	1	ESR1_MOUSE	P19785 mus musculu
42	436	9.9	600	1	ESR1_RAT	P06211 rattus norv
43	431.5	9.8	568	1	ESR2_ONCMY	P57782 oncorhynch
44	427	9.7	557	1	ESR2_ORENI	O9YH32 oreochromis
45	425	9.6	530	1	ESR2_RAT	P062986 rattus norv

## ALIGNMENTS

RESULT 1

ID	MCR_HUMAN	STANDARD	PRT	984 AA.
AC	P08235:			
DT	01-AUG-1988 (Rel. 08, Created)			
DT	01-AUG-1988 (Rel. 08, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Mineralocorticoid receptor (MR).			
GN	NR3C2 OR MLR OR MCR.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=87263386; PubMed=3037703;			
RA	Arriza J.L., Weinberger C., Cereilli G., Glaser T.M., Handelin B.L.,			
RA	Housman D.E., Evans R.M.;			
RT	"Cloning of human mineralocorticoid receptor complementary DNA:			
RT	structural and functional kinship with the glucocorticoid receptor.";			
RL	Science 237:268-273(1987).			
CC	-I- FUNCTION: RECEPTOR FOR BOTH MINERALOCORTICOIDS (MC) SUCH AS			
CC	ALDOSTERONE AND GLUCOCORTICOIDS (GC) SUCH AS CORTICOSTERONE OR			
CC	CORTISOL. THE EFFECT OF MC IS TO INCREASE ION AND WATER TRANSPORT			
CC	AND THUS RAISE EXTRACELLULAR FLUID VOLUME AND BLOOD PRESSURE AND			
CC	LOWER POTASSIUM LEVELS.			
CC	-I- SUBCELLULAR LOCATION: Nuclear.			
CC	-I- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,			
CC	A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.			
CC	-I- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.			
CC	NR3 SUBFAMILY.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (see <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>			
CC	or send an email to <a href="mailto:license@sib-sib.ch">license@sib-sib.ch</a> ).			
CC	-----			
DR	EMBL: M16801; AAA59571.1; -			
DR	PIR: A29513; A29513.			
DR	HSSP: P06536; 1RGD.			
DR	TRANSPAC: T00513; -			
DR	MIM: 600983; -			
DR	InterPro: IPR000536; Hormone_rec_1ig.			
DR	InterPro: IPR001628; zf-C4.			
DR	Pfam: PF00104; hormone_rec.1.			
DR	Pfam: PF00105; zf-C4; 1.			
DR	PRINTS: PR00047; STROIDFINGER.			
DR	SMART: SM00430; HOL1; 1.			
DR	SMART: SM00399; znF_C4; 1.			
DR	PROSITE: PS00031; NUCLEAR_RECEPTOR; 1.			
DR	Receptor: Transcription regulation; DNA-binding; Nuclear protein;			
DR	zinc-finger; Steroid-binding. MODULATING.			
FT	DOMAIN 1 602			

FT DNA\_BIND 603 668 NUCLEAR RECEPTOR-TYPE.  
 FT ZN\_FING 603 623 C4-TYPE.  
 FT ZN\_FING 639 663 C4-TYPE.  
 FT DOMAIN 669 732 HINGE.  
 FT DOMAIN 733 984 STEROID-BINDING.  
 SQ SEQUENCE 984 AA: 107067 MW: 8300CDIA18C1858A CRC64:

Query Match 99.2%; Score 4385; DB 1; Length 984;  
 Best Local Similarity 100.0%; Pred. No. 5..5e-225;  
 Matches 837; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 METKGYHSLPGLDMERWGVSAVERSSLGPERIDENNMYEIVVSCVSGAIPNNST 60  
 1 METKGYHSLPGLDMERWGVSAVERSSLGPERIDENNMYEIVVSCVSGAIPNNST 60  
 DB 1 METKGYHSLPGLDMERWGVSAVERSSLGPERIDENNMYEIVVSCVSGAIPNNST 60  
 OY 61 OGSSKEKOEELPCLOQDNNRPGILTSIDIKTELESKELSATVAESMGLYMDSVRADYSYE 120  
 61 OGSSKEKOEELPCLOQDNNRPGILTSIDIKTELESKELSATVAESMGLYMDSVRADYSYE 120  
 DB 61 OGSSKEKOEELPCLOQDNNRPGILTSIDIKTELESKELSATVAESMGLYMDSVRADYSYE 120  
 OY 121 QONOGSKSPAKIYONVEOLVKFYKNGHREPTSLSCVNTPLRSEMSDSSGSSVNGVMRAI 180  
 121 QONOGSKSPAKIYONVEOLVKFYKNGHREPTSLSCVNTPLRSEMSDSSGSSVNGVMRAI 180  
 DB 121 QONOGSKSPAKIYONVEOLVKFYKNGHREPTSLSCVNTPLRSEMSDSSGSSVNGVMRAI 180  
 OY 181 VKSPIMCEKSPVSCPLNMTSSVCPAGTNSVSTASTSGSPFVHSPITOGPTLTCSPN 240  
 181 VKSPIMCEKSPVSCPLNMTSSVCPAGTNSVSTASTSGSPFVHSPITOGPTLTCSPN 240  
 DB 181 VKSPIMCEKSPVSCPLNMTSSVCPAGTNSVSTASTSGSPFVHSPITOGPTLTCSPN 240  
 OY 241 AENGRSHRSHPAHASNVSPLSSPLSSMKSSISSPSSHCVKSPVSSPNNVTLRSSVSSP 300  
 241 AENGRSHRSHPAHASNVSPLSSPLSSMKSSISSPSSHCVKSPVSSPNNVTLRSSVSSP 300  
 DB 241 AENGRSHRSHPAHASNVSPLSSPLSSMKSSISSPSSHCVKSPVSSPNNVTLRSSVSSP 300  
 OY 301 ANINNSRCSVSPSTNNRSTLSSPAASTVSGICSPVNNASTASGSSASSSTLRDVP 360  
 301 ANINNSRCSVSPSTNNRSTLSSPAASTVSGICSPVNNASTASGSSASSSTLRDVP 360  
 DB 301 ANINNSRCSVSPSTNNRSTLSSPAASTVSGICSPVNNASTASGSSASSSTLRDVP 360  
 OY 361 SPDIOEKAQAEVPPPKTEVESALSNGVTGQUNIVQYIKPEPDGAFSSSCUGNSKINS 420  
 361 SPDIOEKAQAEVPPPKTEVESALSNGVTGQUNIVQYIKPEPDGAFSSSCUGNSKINS 420  
 DB 361 SPDIOEKAQAEVPPPKTEVESALSNGVTGQUNIVQYIKPEPDGAFSSSCUGNSKINS 420  
 OY 421 SSFVPIKOEESTKHSCTSTFRGNPTVNPFPMDGYSIFEMDDKDYLSLIGLPVPGF 480  
 421 SSFVPIKOEESTKHSCTSTFRGNPTVNPFPMDGYSIFEMDDKDYLSLIGLPVPGF 480  
 DB 421 SSFVPIKOEESTKHSCTSTFRGNPTVNPFPMDGYSIFEMDDKDYLSLIGLPVPGF 480  
 OY 481 DGNCGSGEPVGIKQEPDGGSYPPASIPSSAIYVNGSGSEFHRIGAOGTISLSRAR 540  
 481 DGNCGSGEPVGIKQEPDGGSYPPASIPSSAIYVNGSGSEFHRIGAOGTISLSRAR 540  
 DB 481 DGNCGSGEPVGIKQEPDGGSYPPASIPSSAIYVNGSGSEFHRIGAOGTISLSRAR 540  
 OY 541 DQSFQHLSSFPVNTLVESMKS HSGDLSRRSDGYVLEYIPENVSSSTLRSVSTGSSRPS 600  
 541 DQSFQHLSSFPVNTLVESMKS HSGDLSRRSDGYVLEYIPENVSSSTLRSVSTGSSRPS 600  
 DB 541 DQSFQHLSSFPVNTLVESMKS HSGDLSRRSDGYVLEYIPENVSSSTLRSVSTGSSRPS 600  
 OY 601 KICLYCGDEASCHGVYTCGCKAFKRAYGQHNYLCAGNDDIIDIKIRKKNPAPRL 660  
 601 KICLYCGDEASCHGVYTCGCKAFKRAYGQHNYLCAGNDDIIDIKIRKKNPAPRL 660  
 DB 601 KICLYCGDEASCHGVYTCGCKAFKRAYGQHNYLCAGNDDIIDIKIRKKNPAPRL 660  
 OY 661 OKCLOAGMULGARKSKKLGKIGIHEEOPOQOQPPPPPPPOSPPEGTITYIAPAKESVN 720  
 661 OKCLOAGMULGARKSKKLGKIGIHEEOPOQOQPPPPPPPOSPPEGTITYIAPAKESVN 720  
 DB 661 OKCLOAGMULGARKSKKLGKIGIHEEOPOQOQPPPPPPPOSPPEGTITYIAPAKESVN 720  
 OY 721 TALVPOLSTISRALTPSPVWLENTIEPELIVYAGYDSSKPDIAENLSTLNLAGQMIQY 780  
 721 TALVPOLSTISRALTPSPVWLENTIEPELIVYAGYDSSKPDIAENLSTLNLAGQMIQY 780  
 DB 721 TALVPOLSTISRALTPSPVWLENTIEPELIVYAGYDSSKPDIAENLSTLNLAGQMIQY 780  
 OY 781 VMAVVLPEFKKLPLEDQITLLOYSMCLSSPALSMSRYKHNNSOFLVAPLAVNE 837  
 781 VMAVVLPEFKKLPLEDQITLLOYSMCLSSPALSMSRYKHNNSOFLVAPLAVNE 837  
 DB 781 VMAVVLPEFKKLPLEDQITLLOYSMCLSSPALSMSRYKHNNSOFLVAPLAVNE 837

RESULT 2  
 MCR\_TUPGB STANDARD: PRT: 977 AA.  
 ID MCR\_TUPGB  
 AC Q29131; 095268;

DT 01-NOV-1997 (rel. 35, Created)  
 DT 01-NOV-1997 (rel. 35, Last sequence update)  
 DT 01-MAR-2002 (rel. 41, Last annotation update)  
 DE Mineralocorticoid receptor (MR).  
 GN NR3C2 OR MLR.  
 OS Tupia glis belangeri (Common tree shrew).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Scandentia; Tupaiidae; Tupia.  
 OX NCBI\_TaxID=9396;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=98250805; PubMed=9582428;  
 RA Meyer U., Kruehoffer M., Flugge G., Fuchs E.;  
 RT "Cloning of glucocorticoid receptor and mineralocorticoid receptor  
 cDNA and gene expression in the central nervous system of the tree  
 shrew (Tupaia belangeri).";  
 RT Brain Res. Mol. Brain Res. 55:243-253(1998).  
 RN [2]  
 RP SEQUENCE OF 64-431 FROM N.A.  
 RC TISSUE=Colon;  
 RA Kruehoffer M., Klingenberg M., Fuchs E., Forssmann W.G.;  
 RL Submitted (JAN-1995) to the EMBL/Genbank/DBJ databases.  
 CC -1- FUNCTION: RECEPTOR FOR BOTH MINERALOCORTICIDS (MC) SUCH AS  
 CC ALDOSTERONE AND GLUCOCORTICIDS (GC) SUCH AS CORTICOSTERONE OR  
 CC CORTISOL. THE EFFECT OF MC IS TO INCREASE ION AND WATER TRANSPORT  
 CC AND THUS RAISE EXTRACELLULAR FLUID VOLUME AND BLOOD PRESSURE AND  
 CC LOWER POTASSIUM LEVELS (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Nuclear.  
 CC -1- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,  
 CC A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.  
 CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.  
 CC NR3 SUBFAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: Z75077; CA99376.1; -;  
 DR EMBL: X83607; CA958586.1; -;  
 DR HSP: P06536; IRGD.  
 DR InterPro: IPR000536; Hormone\_rec\_119.  
 DR InterPro: IPR001628; zf-C4.  
 DR Pfam: PF00104; hormone\_rec.1.  
 DR Pfam: PF00105; zf-C4.1.  
 DR PRINTS: PR00047; STROIDFINGER.  
 DR SMART: SM00430; HOL1.1.  
 DR SMART: SM00399; ZNF\_C4.1.  
 DR PROSITE: PS00031; NUCLEAR\_RECEPTOR.1.  
 KW Receptor; Transcription regulation; DNA-binding; Nuclear protein;  
 KW Zinc-finger; Steroid-binding.  
 KW ZINC-FINGER; Steroid-binding.  
 FT DOMAIN 1 601 MODULATING.  
 FT DNA\_BIND 602 667 NUCLEAR RECEPTOR-TYPE.  
 FT ZN\_FING 602 622 C4-TYPE.  
 FT ZN\_FING 638 662 C4-TYPE.  
 FT DOMAIN 668 725 HINGE.  
 FT DOMAIN 726 977 STEROID-BINDING.  
 SQ SEQUENCE 977 AA: 106489 MW: 63387CBBF104155F CRC64;

Query Match 90.1%; Score 3985.5; DB 1; Length 977;  
 Best Local Similarity 91.3%; Pred. No. 7.6e-204;  
 Matches 765; Conservative 25; Mismatches 39; Indels 9; Gaps 3;  
 OY 1 METKGYHSLPGLDMERWGVSAVERSSLGPERIDENNMYEIVVSCVSGAIPNNST 60  
 1 METKGYHSLPGLDMERWGVSAVERSSLGPERIDENNMYEIVVSCVSGAIPNNST 60  
 DB 1 METKGYHSLPGLDMERWGVSAVERSSLGPERIDENNMYEIVVSCVSGAIPNNST 60  
 OY 61 OGSSKEKOEELPCLOQDNNRPGILTSIDIKTELESKELSATVAESMGLYMDSVRADYSYE 120  
 61 OGSSKEKOEELPCLOQDNNRPGILTSIDIKTELESKELSATVAESMGLYMDSVRADYSYE 120

```

DB 61 OGSSEKKELOLPCLODQDNQSGILFSEIKTELEPKELSAFVAESMGLYMDVSEADYARE 120
OY 121 OQNOGOSMSPATIQWVEQVYKFGNGRPTSLSCVNTPLASFMSDSSVNGCYMRAI 180
DB 121 OHAQOGSLSPATIQWVEQVLMKFEYGRHRSSTLSNVSPRSPFLPDPSAVNGCYMRAI 180
OY 181 VASPTICHEKSPSCSPLMTTSSVSPAGINSSTTAFSGSPVHSPPTOGPTLCSN 240
DB 181 VASPTICHEKSPSCSPLMTTSSVSPAGINSSTTAFSGSPVHSPPTOGPTLCSN 240
OY 241 AENRGRSRSHSPAHASNVGSPSLSPSSMSKSISSPPSHCSVKSVPYSPNNVTLRSSVSP 300
DB 241 VONRGRSRSHSPAHASNVGSPSLSPSSMSKSISSPPSHCSVKSVPYSPNNVTLRSSVSP 300
OY 301 ANINNSRCVSSPSTNNRSTLSPPAASTVGSICSPVNNAFSTYASGTSGLTDVVP 360
DB 301 ANINNSRCVSSPSTNNRSTLSPPAASTVGSICSPVNNAFSTYASGTSGLTDVVP 360
OY 361 SPDTCEKGOEVPPTKTEVEESAISNGVGLNIYOYIKPEPDGAFSSCLGNSKIND 420
DB 361 SPDTCEKGOEVPPTKTEVEESAISNGVGLNIYOYIKPEPDGAFSSCLGNSKIND 420
OY 421 SSF-SYPIKOEESTKHSCTSGTSEKGNPTVNPFPMDGSYSPFMDKDYISLGLGPVPG 479
DB 421 SSF-SYPIKOEESTKHSCTSGTSEKGNPTVNPFPMDGSYSPFMDKDYISLGLGPVPG 479
OY 479 FGNCEBGTGFPNGIKOEPEYGIYEPASIPSSAIVGNSGGGSHRIGAOGTISLSRBA 538
DB 479 FGNCEBGTGFPNGIKOEPEYGIYEPASIPSSAIVGNSGGGSHRIGAOGTISLSRBA 538
OY 540 ROOSRQHLSSFPVNTLVESMKSNGDLSRRSDGVPVLEYIEPNVSSSLRVSSTSSRP 599
DB 540 ROOSRQHLSSFPVNTLVESMKSNGDLSRRSDGVPVLEYIEPNVSSSLRVSSTSSRP 599
OY 539 ROOSRQHLSSFPVNTLVESMKSNGDLSRRSDGVPVLEYIEPNVSSSLRVSSTSSRP 598
DB 539 ROOSRQHLSSFPVNTLVESMKSNGDLSRRSDGVPVLEYIEPNVSSSLRVSSTSSRP 598
OY 600 SKICLVCGDEAGCHGVVTCGCKKFFKRAVEGQHNLYCAGNDCIIDIKIRKNCPCR 659
DB 600 SKICLVCGDEAGCHGVVTCGCKKFFKRAVEGQHNLYCAGNDCIIDIKIRKNCPCR 659
OY 599 SKICLVCGDEAGCHGVVTCGCKKFFKRAVEGQHNLYCAGNDCIIDIKIRKNCPCR 658
DB 599 SKICLVCGDEAGCHGVVTCGCKKFFKRAVEGQHNLYCAGNDCIIDIKIRKNCPCR 658
OY 660 LOKCLOAGNMLGARRSKILGKLGHEEPQOQPPPPPPQSPPEGTYYIAPAKEPSV 719
DB 660 LOKCLOAGNMLGARRSKILGKLGHEEPQOQPPPPPPQSPPEGTYYIAPAKEPSV 719
OY 659 LOKCLOAGNMLGARRSKILGKLGHEEPQOQPPPPPPQSPPEGTYYIAPAKEPSV 712
DB 659 LOKCLOAGNMLGARRSKILGKLGHEEPQOQPPPPPPQSPPEGTYYIAPAKEPSV 712
OY 720 NTAIVPOLSTIRALTPSPVMTLENIEPIYAGYSSRPDPAENLSTLNLAGQOMIO 779
DB 720 NTAIVPOLSTIRALTPSPVMTLENIEPIYAGYSSRPDPAENLSTLNLAGQOMIO 779
OY 713 NTAIVPOLSTIRALTPSPVMTLENIEPIYAGYSSRPDPAENLSTLNLAGQOMIO 772
DB 713 NTAIVPOLSTIRALTPSPVMTLENIEPIYAGYSSRPDPAENLSTLNLAGQOMIO 772
OY 780 VYKMAKVLPGFKNLPLEDQITLIQYSSMCLSSPALSMSRSTKHTNSOFLYFADPLVNE 837
DB 780 VYKMAKVLPGFKNLPLEDQITLIQYSSMCLSSPALSMSRSTKHTNSOFLYFADPLVNE 837
OY 773 VYKMAKVLPGFKNLPLEDQITLIQYSSMCLSSPALSMSRSTKHTNSOFLYFADPLVNE 830
DB 773 VYKMAKVLPGFKNLPLEDQITLIQYSSMCLSSPALSMSRSTKHTNSOFLYFADPLVNE 830

```

```

RN [2]
RP SEQUENCE OF 689-787 FROM N.A.
RC STRAIN-MISTAR: TISSUE=Cochlea;
RX MEDLINE=95073683; PubMed=7982810;
RA Furuta H., Mori N., Sato C., Hoshikawa H., Sakai S., Iwakura S.,
  DOI K.
RT "Mineralocorticoid type I receptor in the rat cochlea: mRNA
  identification by polymerase chain reaction (PCR) and in situ
  hybridization."
  Hear. Res. 78:175-180(1994).
RN [3]
RP SEQUENCE OF 597-679 FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE=Brain;
RX MEDLINE=96103549; PubMed=7495694;
RA Bloem L.J., Guo C., Prall J.H.,
  "Identification of a splice variant of the rat and human
  mineralocorticoid receptor genes."
  J. Steroid Biochem. Mol. Biol. 55:159-162(1995).
RT - FUNCTION: RECEPTOR FOR BOTH MINERALOCORTICOIDS (MC) SUCH AS
  ALDOSTERONE AND GLUCOCORTICOIDS (GC) SUCH AS CORTICOSTERONE OR
  CORTISOL. THE EFFECT OF MC IS TO INCREASE ION AND WATER TRANSPORT
  AND THUS RAISE EXTRACELLULAR FLUID VOLUME AND BLOOD PRESSURE AND
  LOWER POTASSIUM LEVELS.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- ALTERNATIVE PRODUCTS: TWO FORMS OF THE RECEPTOR ARE PRODUCED
  BY ALTERNATIVE SPLICING.
CC -1- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
  A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
CC NR3 SUBFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
  between the Swiss Institute of Bioinformatics and the EMBL outstation -
  the European Bioinformatics Institute. There are no restrictions on its
  use by non-profit institutions as long as its content is in no way
  modified and this statement is not removed. Usage by and for commercial
  entities requires a license agreement (see http://www.isb-sib.ch/announce/
  or send an email to license@isb-sib.ch).
CC -----
DR EMBL, M36074; AAA41583.1; -
DR EMBL, S75686; AAB32663.2; -
DR EMBL, S79920; AAB35738.1; -
DR PIR, A41401; A41401.
DR HSP, P06536; IRGD.
DR TRANSFAC; T00511; -
DR InterPro; IPR000536; Hormone_rec_1lg.
DR InterPro; IPR001628; zf-C4.
DR Pfam; PF00104; hormone_rec; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR00047; STEROIDFINGER.
DR SMART; SM00399; ZNF_C4; 1.
DR SMART; SM00430; HOL1; 1.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
KW Receptor: Transcription regulation; DNA-binding; Nuclear protein;
  Zinc-finger; Steroid-binding; Alternative splicing.
FT DOMAIN 1 603
FT DNA_BIND 604 669 NUCLEAR RECEPTOR-TYPE.
FT ZN_FING 604 624 C4-TYPE.
FT ZN_FING 640 664 C4-TYPE.
FT DOMAIN 670 729 HINGE.
FT DOMAIN 730 981 STEROID-BINDING.
FT VARSPPLIC 634 634 G -> GKCSW (IN SECOND ISOFORM).
FT CONFLICT 771 771 A -> G (IN REF. 2).
FT CONFLICT 775 775 I -> S (IN REF. 2).
SQ SEQUENCE 981 AA; 106737 MW; 184F5D37C1B030F7 CRC64;

```

```

Query Match 88.6%; Score 3919.5; DB 1; Length 981;
Best Local Similarity 89.0%; Pred. No. 2.4e-200;
Matches 746; Conservative 35; Mismatches 52; Indels 5; Gaps 2;
1 MEKYGHSLEPGEDMRRGQVSOAVERSSLPTEPTDENNYMEIYVNCVSGAIPNNST 60
|||||

```

```

Db 1 METGYHSLPGLDMERRMSVQSLTERRSISGPARETTENNMYETIVNVCYSGLAIPNNST 60
QY 61 QGSSKEKELLPCLOODNNRPGIILTSIDIKTELSEKELSAIVAESMGILYMSVRADADSYE 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 QGSSKEKELLPIQODNSRGILLPSIDIKTELSEKELSAIVAESMGILYMSVRADAEYTD 120
QY 121 QONOGSMPAKIYONVQLYFKFKGNHRSTLSVCVPTLRSPMSDGSVNGVGMAL 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 QONOGSLSPKIKYONMOLVFKYKENGHRSTLSVMSRPLRSPMSDGAASMGALALAI 180
QY 181 VKSPIMCHEKSPVCSPLNMTSVCSPPAGINSVSTAFSGSPFVHSPITOTGTLCSPN 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 VKSPITCHEKSSVSPPLNMASSVCSPPGINSMSSTTSPFSPVHSPITOTGTLCSPS 240
QY 241 AENRGRSHSPAHASNVCSPLSSPLSMKSSITSPSPHCSYKSPVSPNNNTLASSVSP 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 VENRGRSHSPTHASNVCSPLSSPLSMKSPITSPSPHCSYKSPVSPNNNTLASSVSP 300
QY 301 ANINNSRCSVSSPS - NTNNRSTLSPASTVSGISCPYNNNAFSYASGTSAGSSTLRDPV 359
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 301 ANLNNSRCSVSSPSNNNTNRSTLSPASTVSGISCPISMAFSTATSCASAGACAIQDYN 360
QY 360 PSPDIOEKGAEVPEPKTEEVESALSNVGTQLNTVOYIKPEPDGAFSSSCLIGNSKINS 419
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 361 PSPDHEKGAHDVPEPKTEEVESKALSNVGTGPLNTVOYIKSEPDGAFSSSCLIGNSKISP 420
QY 420 DSSFSVPTKQESTKHSCTSGTSGKGNPTVNPFPNMGSTFSFMDKDYSLSGTILGPPVG 479
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 421 SSPFSVPTKQESSKHSCTSGASFGKGNPTVNPFPNMGSTFSFMDKDYSLSGTILGPPVG 480
QY 480 FPGNCEGSGFPGIKQEPDGSYYPEASIPSSAIVGNSGGSGSFYRIGAGGTISLSRSA 539
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 481 FPGSCEDSAFPGIKQEPDGSYYPEASIPSSAIVGNSGGSGSFYRIGAGGTISLSRSP 540
QY 540 RQDSFOHLSFPFVNTLVESMKSHEGDLSSRRSDGYPLVLEYIPENVSSTLRSVSTGSSRP 599
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 541 RQDSFOHLSFPFVNTLVESMKSHEGDLSSRRSDGYPLVLEYIPENVSSTLRSVSTGSSRP 600
QY 600 SKTICLVCGDEASGCHGYVTCGCKVFEKRAVEGQHNHYLCAGRNCCIIDKIRKNCPCR 659
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 601 SKTICLVCGDEASGCHGYVTCGCKVFEKRAVEGQHNHYLCAGRNCCIIDKIRKNCPCR 660
QY 660 LQKCLQAGNNLGAARKSKLGLKGLGHEEQPOOQPPPPPPPOSPDEGTTYIAPAKEPSV 719
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 661 LQKCLQAGNNLGAARKSKLGLKGLGHEEQPOOQPPPPPPPOSPDEGTTYIAPAKEPSV 716
QY 720 NIALVPOLSTISRALTPSPVAVLENTIEPIVYAGYDSSKPDIAENLSTLNRLAKQOMIQ 779
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 717 NSALVPOLSTISRALTPSPVAVLENTIEPIVYAGYDSSKPDIAESLSTLNRLAAQOMIQ 776
QY 780 VYVMAVVLPGFKMLPLEDQITLLOYSWMGLSPFALSMSRYKHTNSOLFAPDLVENE 837
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 777 VYVMAVVLPGFKMLPLEDQITLLOYSWMGLSPFALSMSRYKHTNSOLLYFAPDLVENE 834

```

```

CC -1- FUNCTION: RECEPTOR FOR BOTH MINERALOCORTICOIDS (MC) SUCH AS
CC ALDOSTERONE AND GLUCOCORTICOIDS (GC) SUCH AS CORTICOSTERONE OR
CC CORTISOL. THE EFFECT OF MC IS TO INCREASE ION AND WATER TRANSPORT
CC AND THUS RAISE EXTRACELLULAR FLUID VOLUME AND BLOOD PRESSURE AND
CC LOWER POTASSIUM LEVELS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
CC A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
CC NR3 SUBFAMILY.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
CC EMBL: U15133; AAA75574.1; -.
CC EMBL: U15135; AAA75575.1; -.
CC HSSP: P06536; IRGD.
CC InterPro: IPR000536; Hormone_rec_1lg.
CC InterPro: IPR001628; zf-C4.
CC Pfam: PF00104; hormone_rec_1.
CC Pfam: PF00105; zf-C4; 1.
CC SMART: SM00430; HOL1; 1.
CC SMART: SM00399; znf-C4; 1.
CC PROSITE: PS00031; NUCLEAR_RECEPTOR; 1.
CC Receptor; Transcription regulation; DNA-binding; Nuclear protein;
CC Zinc-finger; Steroid-binding.
CC NON_TER 1
CC DOMAIN <1 228 MODULATING.
CC FT DNA_BIND 229 298 NUCLEAR RECEPTOR-TYPE.
CC FT ZN_FING 229 249 C4-TYPE.
CC FT ZN_FING 269 293 C4-TYPE.
CC FT DOMAIN 299 360 HINGE.
CC FT DOMAIN 361 612 STEROID-BINDING.
CC SEQUENCE 612 AA; 67946 MW; CDD66DDC0A5FBA08 CRC64;

Query Match 39.9%; Score 1763.5; DB 1; Length 612;
Best Local Similarity 72.1%; Pred. No. 1.7e-86;
Matches 338; Conservative 57; Mismatches 51; Indels 23; Gaps 8;

QY 392 INIVQYIKPEPDGAFSSSCLIGNSKINSSEFSYPIKQESTKHSCTSGTSGKGNPTVNPFP 451
    :::::||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 9 VSLVAFIRPDPAIFSSGCFG--DTVSSDPAFSLPIKQESCKNTCCSALFKGQSASMPFP 66
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 452 FMDGYSFSPMDKDYISLSGLIGPPVPGFDGNCESGFP-----YGIKQEPDGSYYPEA 506
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 67 FMDGYSYFAFMDKDYISLSGLIGPPVSGFDGFCNGCSNGLNVALKQETEDSSFFPEN 126
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 507 STPSSAIVGNSGGSGSFYRIGAGGTISLSRSA--RDOSFOHLSFPFVNTLVESMKSHEG 565
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 127 NMPSSAIVGNSGGSGSFYRIGAGGTISLSRPLNRDGSFQNLSEFPSPSSILVESMKTQSE 186
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 566 -----LSRRSDGYPLVLEYIPENVSSTLRVSYSGSSRPSTICLVCGDEASGCHGYVTC 620
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 187 LAQNTLSSRRNDGFPVPGTIEPNNMSTTLRSMSTSPSRKVCYLVCGDEASGCHGYVTC 246
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 621 GSKVYFFKRAVGE---QHNTYLCAGRNCCIIDKIRKNCPCRQKCLQAGMNLGAARKSK 676
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 247 GSKVYFFKRAVGEKSRSHSYLCAGRNCCIIDKIRKNCPCRQKCLQAGMNLGAARKSK 306
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 677 KIGKLKGLGHEEQPOOQPPPPPPPOSPDEGTTYIAPAKEPSVNT-ALVPOLSTISRALT 735
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 307 KIGKLKGLGHEEQPOO---PLQOPTPASPEKEDTTLTSSKEPSANSLVPLISAIPALIT 363
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 736 PSPVAVLENTIEPIVYAGYDSSKPDIAENLSTLNRLAGQOMIQVYVMAVVLPGFKMLPL 795
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 364 LSAVAVLENTIEPIVYAGYDNTQPTAENLSTLNRLAGQOMIQVYVMAVVLPGFKMLPL 423

```



OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86092206; PubMed=2867473;  
 RA Hollenberg S.M., Weinberger C., Ong E.S., Cerelli G., Oro A.,  
 RA Lebo R., Thompson E.B., Rosenfeld M.G., Evans R.M.;  
 RT "Primary structure and expression of a functional human  
 RT glucocorticoid receptor cDNA.";  
 RL Nature 318:635-641(1985).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).  
 RX MEDLINE=91201378; PubMed=207881;  
 RA Encio I.J., Deterra-Wadleigh S.D.;  
 RT "The genomic structure of the human glucocorticoid receptor.";  
 RL J. Biol. Chem. 266:7182-7188(1991).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Munroe D.G., Pang J., Taylor G.R., Lau C., Planter R.K., Zhou L.;  
 RL Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE OF 1-394 FROM N.A.  
 RX MEDLINE=91224961; PubMed=2026589;  
 RA Leclerc S., Xie B.X., Roy R., Govindan M.V.;  
 RT "Purification of a human glucocorticoid receptor gene promoter-binding  
 RT protein. Production of polyclonal antibodies against the purified  
 RT factor.";  
 RL J. Biol. Chem. 266:8711-8719(1991).  
 RN [5]  
 RP SEQUENCE OF 396-630 FROM N.A.  
 RA Kimmery W., Bondoc M., Cheng J., Connolly K.S., Gunning K.M.,  
 RA Kader K., Miguel T., Miller C., Pitluck S., Pollard M., Rojeski H.,  
 RA Subramanian S., Martin C.H.;  
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP DOMAINS.  
 RX MEDLINE=86092211; PubMed=3841189;  
 RA Weinberger C., Hollenberg S.M., Rosenfeld M.G., Evans R.M.;  
 RT "Domain structure of human glucocorticoid receptor and its  
 RT relationship to the v-erb-A oncogene product.";  
 RL Nature 318:670-672(1985).  
 RN [7]  
 RP VARIANT SER-363.  
 RX MEDLINE=93187003; PubMed=8445027;  
 RA Karl M., Lamberts S.W.J., Deterra-Wadleigh S.D., Encio I.J.,  
 RA Stratakis C.A., Hurley D.M., Accili D., Chrousos G.P.;  
 RT "Familial glucocorticoid resistance caused by a splice site deletion  
 RT in the human glucocorticoid receptor gene.";  
 RL J. Clin. Endocrinol. Metab. 76:683-689(1993).  
 RN [8]  
 RP VARIANT VAL-641.  
 RX MEDLINE=91123468; PubMed=1704018;  
 RA Hurley D.M., Accili D., Stratakis C.A., Karl M., Vamvakopoulos N.,  
 RA Rorer E., Constantine K., Taylor S.I., Chrousos G.P.;  
 RT "Point mutation causing a single amino acid substitution in the  
 RT hormone binding domain of the glucocorticoid receptor in familial  
 RT glucocorticoid resistance.";  
 RL J. Clin. Invest. 87:680-686(1991).  
 RN [9]  
 RP VARIANT ILE-729.  
 RX MEDLINE=93253031; PubMed=7683692;  
 RA Melchhoff D.M., Brufsky A., Reardon G., McDermott P., Javier E.C.,  
 RA Bergh C.H., Rowe D., Melchhoff C.D.;  
 RT "A mutation of the glucocorticoid receptor in primary cortisol  
 RT resistance.";  
 RL J. Clin. Invest. 91:1918-1925(1993).  
 RN [10]  
 RP VARIANT PHE-753.  
 RX MEDLINE=93302771; PubMed=8316249;  
 RA Astral J., Thompson E.B.;  
 RT "Identification of the activation-labile gene: a single point mutation

RT in the human glucocorticoid receptor presents as two distinct receptor  
 RT phenotypes.";  
 RL Mol. Endocrinol. 7:631-642(1993).  
 RN [11]  
 RP VARIANTS HIS-477 AND SER-679.  
 RX PubMed=11589680;  
 RA Nilsson L., Lind U., Gafvels M., Eggertsen G., Carlstedt-Duke J.,  
 RA Nilsson L., Holtmann M., Stelma P., Wikstrom A.C., Werner S.;  
 RT "Characterization of two novel mutations in the glucocorticoid  
 RT receptor gene in patients with primary cortisol resistance.";  
 RL Clin. Endocrinol. (Oxf) 55:363-371(2001).  
 CC -I- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN  
 CC THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR  
 CC PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES. BINDS TO THE  
 CC GRE TARGET SITE.  
 CC -I- SUBCELLULAR LOCATION: Nuclear.  
 CC -I- ALTERNATIVE PRODUCTS: 2 ISOFORMS, ALPHA (SHOWN HERE) AND BETA; ARE  
 CC PRODUCED BY ALTERNATIVE SPLICING. ALPHA-HGR IS THE PREDOMINANT  
 CC PHYSIOLOGICAL FORM OF HGR. THE IN VITRO TRANSLATION PRODUCT OF HGR  
 CC BETA DOES NOT BIND STEROID ITS FUNCTION IS UNCLEAR; HOWEVER, IT IS  
 CC POSSIBLE THAT VARIANT RECEPTORS PERFORM TISSUE-SPECIFIC FUNCTIONS.  
 CC -I- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,  
 CC A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.  
 CC -I- DISEASE: DEFECTS IN NR3C1 ARE A CAUSE OF FAMILIAL GLUCOCORTICOID  
 CC RESISTANCE (CORTISOL RESISTANCE); A HYPERTENSIVE, HYPERANDROGENIC  
 CC DISORDER CHARACTERIZED BY INCREASED SERUM CORTISOL CONCENTRATIONS.  
 CC -I- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.  
 CC NR3 SUBFAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (see <http://www.isb.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: M10901; AAA52521.1; -;  
 DR EMBL: X03225; CAA26976.1; -;  
 DR EMBL: X03348; CAA27054.1; -;  
 DR EMBL: U80946; AAB64353.1; JOINED.  
 DR EMBL: U78506; AAB64353.1; JOINED.  
 DR EMBL: U78507; AAB64353.1; JOINED.  
 DR EMBL: U78508; AAB64353.1; JOINED.  
 DR EMBL: U78510; AAB64353.1; JOINED.  
 DR EMBL: U78511; AAB64353.1; JOINED.  
 DR EMBL: U78512; AAB64353.1; JOINED.  
 DR EMBL: U80947; AAB64354.1; JOINED.  
 DR EMBL: U78506; AAB64354.1; JOINED.  
 DR EMBL: U78507; AAB64354.1; JOINED.  
 DR EMBL: U78508; AAB64354.1; JOINED.  
 DR EMBL: U78509; AAB64354.1; JOINED.  
 DR EMBL: U78510; AAB64354.1; JOINED.  
 DR EMBL: U78511; AAB64354.1; JOINED.  
 DR EMBL: U78512; AAB64354.1; JOINED.  
 DR EMBL: U01351; AAA16603.1; -;  
 DR EMBL: M69104; AAA88049.1; -;  
 DR EMBL: M7816; AAA53151.1; -;  
 DR EMBL: S68378; AAB20466.1; -;  
 DR EMBL: AC005601; AAC34207.1; -;  
 DR PIR: A03246; ORHUGA.  
 DR PIR: A03247; ORHUGB.  
 DR HSSP: P06536; 1GDC.  
 DR TRNSPAC: T00337; -;  
 DR MIM: 138040; -;  
 DR InterPro: IPR001409; Glucocorticd\_receptor.  
 DR InterPro: IPR000536; Hormone\_rec\_1lg.  
 DR InterPro: IPR001628; zf-C4.  
 DR Pfam: PF02155; GCR; 1.  
 DR Pfam: PF00104; hormone\_rec; 1.  
 DR Pfam: PF00105; zf-C4; 1.  
 DR PRINTS: PR00047; STEROIDFINGER.





05 Aotus nancymae (Owl monkey).  
06 Craniata; Vertebrata; Euteleostomi;  
0C Eukaryota; Metazoa; Chordata;  
0C Mammalia; Primates; Platyrrhini; Cebidae; Aotinae; Aotus

RC	RP	RN	SEQUENCE FROM N.A.	TISSUE=Liver;
			[1]	

RT squirrel monkey (*Saimiri boliviensis boliviensis*), a glucocorticoid receptor-positive primate".

CC -1- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN  
CC THE REGULATION OF EMBRYONIC GENE EXPRESSION AND AFFECT CELLULAR  
CC PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES. BINDS TO THE  
CC

CC -1- SUBCELLULAR LOCATION: Nuclear.  
CC -1- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,  
CC A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.  
CC -1- FUNCTION: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.  
CC -1- TISSUE SPECIFICITY: EXPRESSED IN THE NUCLEUS OF THE

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation.

CC the European Bioinformatics Institute. There are no restrictions on  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or Send an email to [licensing@bio.com](mailto:licensing@bio.com).  
CC -----  
DR EMBL; U07952; AAC51132.1; -  
DR HSSP; P06536; IGDC.  
DR InterPro: IPR001409: Glucocorticoid receptor.  
DR -----

```
DR InterPro; IPR000536; Hormone_rec_1lg.
DR InterPro; IPR001628; zf-C4.
DR Pfam; PF02155; GCR; 1.
DR Pfam; PF00104; hormone_rec; 1.
```

DR PI4K; PIP3K; ZIK-4; 1.  
DR PRMT5; PRMT6; SPINDLING.  
DR SMART; SMO430; HOL1; 1.  
DR SMART; SMO339; ZIK-4; 1.  
DR PROSTATE; PSN0031; NUCLEAR RECEPTOR; 1.  
DR

KM	Receptor; Transcription regulation; DNA-binding; Nuclear protein;
KM	Zinc-finger; Steroid-binding.
PT	DOMAIN 1 420 MODULATING.
PT	DNA_BIND 421 486 NUCLEAR RECEPTOR-TYPE.

SC	SEQUENCE	777 AA	85623 MW	8E20018750184203 CRC64
FT	ZN_FING	421	441	C4-TYPE.
FT	ZN_FING	457	481	C4-TYPE.
FT	DOMAIN	487	527	HINGE.
FT	DOMAIN	528	777	STEROID-BINDING.

Query Match	19.3%	Score 853;	DB 1;	Length 777;
Best Local Similarity	30.5%	Pred. No. 3.5e-38;		

[illegible][illegible]

QY	139 QLYKFKNGHPRPLSCVNTPLRSPMSDSSSYNGSWRAIKSPIMCHESPSVCSP.L	198
	: : :	:
Db	124 EST-----ANL	129

```

QY 199 NMSSVCSCEAGLINSVSTTASFGSPVPHSPITGCTPLTCSPMNENKSNHSAHANSNG 258
    |::| |::|
Db 130 NRSTVPE---NPKSSASSSVSAAP-----KEKEPPTH----- 160

```

OY		259	SPLSSPILSMKMSSTISSPPSCSVSKSPVSSPNNTLLRSSVSYPANI--NNSRCGVSSPSMTN	317
Db		161	SDVSSSEDONLKGQTG-----TNGGNKKLYTAQDSFTDILLQDLFEFGSGPKET	208
OY		318	NRSFLSSPAASTVASICSPV-NNAFSYTASGTSAQSSTLRDVVP--SPPTOKGAQEVPF	374
Db		209	NOSWRBDLLIDENCILSLPAGEDBSFLEGNIN-----EDCKPLILPPTK-----	254
OY		375	PRTVEESAISSNGVTGOLNIIVQYIKPEPDGAESSCLGNSKINSDFSFPV-IKEOSTK	433
Db		255	PKRID-----NGDLVLSSSNVTLPOVKTEK--	280
OY		434	HSCGSTFKKNPIYNPPREFMDSFSFMDDKOYLSGLGPFPVPGFDNCGSGSFFPYGI	493
Db		281	-----EDFIELC-----TPCV-----I	292
OY		494	KOEPPDGSYYPEASISPSAIVG-----VNSGGSPHYRIGAOGTISLSRSARDQ	542
Db		293	KOE-KLSTVYCQASFPCGANIYGKMSAISLHGVSSTGGGMHYDM--NTASTSQ-QDG	347
OY		543	SFOHLSSFPPVNTLVSEW---KSHGD--LSSRSDCGYPLELEYIPENVSSTLR-----	590
Db		348	K-PLEFNVIPIPLPGSEMWNRCOSSGSDNLTSLETLPFPERTVFSMGYSSPSRMPDYSSPP	406
OY		591	-SVSTGSS-PPRKICLCVCGEAGSCGHYGVYTGCSCVFERRAVEGOHNLCGRNDCTID	648
Db		407	SSSTATATGPPKLCLVCSEBAGCHGVLTGSCCVFFRAVEGOHNYLCGRNDCTIID	466
OY		649	KIRRNCPACRLCKLOLAGNMIGARRSKKLGKLTIEHQPOOQQPPPPPPOSPEGST	708
Db		467	KIRRNCPACRYRKCLOAGNLEARKTKK--KIKKI-----QQAT	504
OY		709	TYIA-PAKESVNTALVPLQSTISRALTSPBVAVLENIEPELYIAGYDSKRDTEANLIS	767
Db		505	TGVSQETSENPANKTIYP-ATLPQ-LTPLVSLLEVIEPEVLAYGYSTVDSTWRIMT	561
OY		768	TLNLTACKOMIQVAKVAKVIFGPFKNLPLEQOTLILOYSMWCSSFPALSRSVKHNSOFU	827
Db		562	TLNLTGGROYIAAVKAKKAIFGRFNHLHDDQMLLOYSMFLMAFRALGKRSTRQASSNUL	621
OY		828	YFAPDLVENE	837
Db		622	CFADPLINE	631
<hr/>				
RESULT	9			
GCR_SAIBB	ID	GCR_SAIBB	STANDARD;	PRT; 777 AA.
AC		013186;		
DT		15-JUL-1998 (Rel. 36, Created)		
DT		15-JUL-1998 (Rel. 36, Last sequence update)		
DT		16-OCT-2001 (Rel. 40, Last annotation update)		
DE		Glucocorticoid receptor (Gr).		
NN		NR3C1 OR GR.		
OS		Saimiri boliviensis boliviensis (bolivian squirrel monkey).		
OC		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
CC		Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.		
OX		NCBI_taxid=39432;		
RN		{1}		
RP		SEQUENCE FROM N.A.		
RC		TISSUE=Liver;		
RX		MEDLINE=97117669; PubMed=9024238;		
RA		Reynolds P.D., Pittler S.J., Scammell J.G.;		
RT		*Cloning and expression of the glucocorticoid receptor from the		
RT		squirrel monkey (Saimiri boliviensis boliviensis), a glucocorticoid-		
RT		resistant primate.*;		
RL		J. Clin. Endocrinol. Metab. 82:465-472(1997).		
CC		-1- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN		
CC		PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES. BINDS TO THE		
CC		GRE TARGET SITE.		
CC		-1- SUBCELLULAR LOCATION: Nuclear.		

```

CC      -I- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
CC      A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
CC      -I- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
CC      NR3 SUBFAMILY.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (see http://www.isb-sib.ch/announcement/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL: U87951; AAC51131.1; -.
DR      HSSP: P06536; 1GDC.
DR      InterPro: IPR001409; Glucocorticd_receptor.
DR      InterPro: IPR000536; Hormone_rec_1lg.
DR      InterPro: IPR001628; zf-C4.
DR      Pfam: PF02155; GCR. 1.
DR      Pfam: PF00104; hormone_rec. 1.
DR      Pfam: PF00105; zf-C4; 1.
DR      PRINTS: PR00047; STEROIDFINGER.
DR      SMART: SM00430; HOL1. 1.
DR      SMART: SM00399; ZNF_C4; 1.
DR      PROSITE: PS00031; NUCLEAR_RECEPTOR; 1.
DR      Receptor; Transcription regulation; DNA-binding; Nuclear protein;
KW      Zinc-finger; Steroid-binding.
FT      DOMAIN 1 420 MODULATING.
FT      DNA_BIND 421 486 NUCLEAR RECEPTOR-TYPE.
FT      ZN_FING 421 441 C4-TYPE.
FT      ZN_FING 457 481 C4-TYPE.
FT      ZN_FING 487 527 HINGE.
FT      DOMAIN 528 777 STEROID-BINDING.
SQ      SEQUENCE 777 AA; 85611 MW; CE3CD9EDB64AF3AB CRC64;

Query Match 19.3%; Score 853; DB 1; Length 777;
Best Local Similarity 30.6%; Pred. No. 3.5e-38;
Matches 260; Conservative 103; Mismatches 225; Indels 262; Gaps 32;

QY      28 RSSLPTERTEDNNNM--EIVNVCVSGAIPNNSTOGSSKEKQELLPLCLQDNNRPGILT 85
DB      4 KSLTLPGEKEENSVLTQERGVNMPDCKILKCATLKAVSVSTSLAASQSDSKOORLIV 63
QY      86 SDIK--TELESKELSATVAEESGLYIM--DSVRDADYSEQQNQOGSMSPAKIYQWVE 138
DB      64 DPPKGSYSNAQOPDLSKAVSLSMGLYMGETEYKVMGNLDGFQOQOISLSGETLQILLE 123
QY      139 QLVKFFYKGNHRPSTLSCVNTPLRSFMSDGSVNGVMAIKSPIIMCHEKSPSVCPL 198
DB      124 ESI-----MODLVLSSSNVTLTPQVTKER-- 129
QY      199 NMTSSVCSFAGINSVSTTASFGSEFPVHSPTIQGTPLICSPAENKGRSHSPAHASVNG 258
DB      130 NSTSTPVE--NPKRSSASSVSAA--KEKEFPKTH----- 160
QY      259 SPLSPSLSSMKSSISSPHCSKVPVSSPNVTLRSSVSPSPANI--NNSRCVSSPSMTN 317
DB      161 SVYSSBOQNLKQQT-----SNGVAKIYTDQSTFDLQDLQLETSFGSPKQET 208
QY      318 NSTSLSPASTVSGISCFV--NNAFSYTAAGSAGSSTLRDVP--SPDTEKGAQEVPF 374
DB      209 NQSPMKSDLLIDENCLLSPLAGEDDSFLLEGNSN--EDCKPLILDPDK----- 254
QY      375 PTEVEEASAINSGVTGQNLTIYVIRPEPDGAFSSSCGLGKNSKINDSSSEFV--IQESTK 433
DB      255 PKIKD-----MODLVLSSSNVTLTPQVTKER-- 280
QY      434 HSCSGSFKGNFTVNPFPMDGSEYFSPMDKDYISLISGLPVPYGPQNGCGSGFPVGI 493
DB      281 -----EDFIELC-----TPGV-----I 292
QY      494 KOEPDGGSYPEASIPSSAIVG-----VNSGGSFHYRIGAGQITLISRSARDO 542

```



```

Db 456 NDCIIDKIRENCPACRYRCKLQAGNMLQARKTK--KIKGI----- 495
QY 703 SPEEGTYIAAPKPEVSVALPOLSTISRALTSPVWMLNIEPIVYAGYDSSKPDPA 762
Db 496 --QOATGVQSMTSEMPKTIYP--ATLPQ-LTPPLVSLLEVIEPIVHSGVDSIPSDST 550
QY 763 ENILSTLNLAQKQMIQVYKAKVLPFGKNLPLEDOITLIQYSNMCLSSFSALSWRSYKHT 822
Db 551 WKIMTTLNMLGKROYIAAVKAKAIPGFKNLHLDQMTLLQTSWMTLAFALGWSYKOS 610
QY 823 NSQFLYPADLVFNE 837
Db 611 NGSILCFAPDLTINE 625

RESULT 11
GCR_PIG STANDARD: PRT: 703 AA.
AC Q9NUJ3; O9GKZ9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Glucocorticoid receptor (GR) (Fragment).
GN NR3C1 OR GR.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN 11
RP SEQUENCE FROM N.A.
RC Tissue-Liver:
RA Gutschner M., Eder S., Mueller M., Claus R.;
RT "Porcine glucocorticoid receptor - sequencing, cloning, recombinant
expression and raising a antiserum.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
CC - FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN
THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR
PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES. BINDS TO THE
GRE TARGET SITE (BY SIMILARITY).
CC - SUBCELLULAR LOCATION: Nuclear (By similarity).
CC - DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
CC - SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
NR3 SUBFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF141371; AAF66595.1; -
DR EMBL; AJ296022; CAC10271.1; -
DR InterPro; IPR001409; Glucocorticoid_receptor.
DR InterPro; IPR000536; Hormone_rec_119.
DR InterPro; IPR001723; Steroidhormone_receptor.
DR InterPro; IPR001628; zf-C4.
DR Pfam; PF02155; GCR. 1.
DR Pfam; PF00104; hormone_rec. 1.
DR Pfam; PF00105; zf-C4. 1.
DR PRINTS; PR000398; STRDHOMONER.
DR PRINTS; PR00047; STROIDFINGER.
DR SMART; SM00430; HOL. 1.
DR SMART; SM00399; znF_C4. 1.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR. 1.
KW Receptor; Transcription regulation; DNA-binding; Nuclear protein;
zinc-finger; Steroid-binding.
FT NON_TER 1
FT DOMAIN <1 384 MODULATING.
FT DNA_BIND 385 450 NUCLEAR RECEPTOR-TYPE.
FT C4_TYPE 385 405
FT ZN_FING 385 405

```

```

FT ZN_FING 421 445 C4-TYPE.
FT DOMAIN 451 491 HINGE.
FT NON_TER 492 >703 STEROID-BINDING.
FT SEQUENCE 703 AA; 76637 MW; EBD928DDE8EBC26 CRC64;

Query Match 19.2%; Score 847.5; DB 1; Length 703;
Best Local Similarity 31.2%; Pred. No. 6,1e-38;
Matches 254; Conservative 92; Mismatches 194; Indels 275; Gaps 32;

QY 71 LPLQODNNRPILTSIDIK-----TELESKELSATVAESGLYM---DSVRADYSYEQO 122
Db 8 LAASQPDSDKQQLAVDPFKGSGSNQOPDLKAVSLSGVLMTGETETVYMSDGLGFPQO 67
QY 123 NOGGSNPAKTIYONVEQLVKYKGNGRDPTSLCVNTPLRSEFMSDSSGVNCGVMRAIVK 182
Db 68 GO-----ISLSGETDR-----LLE 83
QY 183 SPLMCHKSPSYCSPLNMTSSVCSAGINSVSTTSFCSFVHSPITGCTPLTCSPMNE 242
Db 84 ESTIANLSRSTVPEPKSSASAGPA-----AAEKAEPKTHSDGA- 124
QY 243 NGRSGHSPAHASNVGSPILSPSSMKSSISSPSHCSYKSPV--SSPNVTLRSSVSPA 301
Db 125 -----PEQPNVKGQTGTNGGVNKLFTTDQSTF 151
QY 302 NINNSRC-SVSPSNTNNRSTLSSPASTV---GSICSPVNNAFSYTASGTG---AG 351
Db 152 DIWRKKLDLELPSCSGPKETSESPWSSDLLIDENCLLSP-----AGEEDPFLBG 203
QY 352 SSTLRVVP--SPDQEKAAQEVPPPKTEEVESAIANGYTGQNLVQYIKRPDGAFFSS 409
Db 204 SST-EDCKPLVLPDK-----PKVKD-----ELLIPSPN----- 233
QY 410 CIGGNSKINSDSSESVPIKQESTKHSCGSTSFKNPTVNPFPFMDGSYSPMDKDYSL 469
Db 234 -----SVPLQVKT-----EKEDFIEL 250
QY 470 SGLIPVPDGFPGNCGSGFPVGIKQEPDGSYYPEASIPSSAIVG-----VNS 518
Db 251 C-----TPGV-----IKOE-KLGPAYCQAFSGANIGKMSAISVHGVS 291
QY 519 GGOSFYRIGAGCTISLSASARDQSFQHLSSPPVTVLVEW---KSHD----- 565
Db 292 GQOLVHYDMNTAASLSKQOEORPL---PNVIPPVIGSENNRRCGSGDDMLTSLGTLN 347
QY 566 LSSRR--SDGYPLVEYIPENVSSSTLRVSSTGSSRPSKICLVGDEASGCHGVVTCGSG 623
Db 348 FGRGSYFSNGISPGMRPDPVSSPPSSSAATGP--PPKILCVCSDEASGCHGVLTGCGS 405
QY 624 KYFFKRAVEGQHNHYLCAGRNDICIIRKKNCPACRLQRCLOAGNMLGARKSKKLGKLG 683
Db 406 KYFFKRAVEGQHNHYLCAGRNDICIIRKKNCPACRYRCKLQAGNMLQARKTK--KIKG 463
QY 684 THEEQOQOQPPPPPPPSPEEGTYIA-PAKPEVSVALPOLSTISRALTSPVWML 742
Db 464 I-----QOATGVQSMTSEMPKTIYP--ATLPQ-LTPPLVSL 500
QY 743 ENIEPIVYAGYDSSKPDPAENILSTLNLAQKQMIQVYKAKVLPFGKNLPLEDOITLI 802
Db 501 EYIEPEVLYAGYDSSIPSDTWTIRMTALNMLGKROYIAAVKAKAIPGFKNLHLDQMTLL 560
QY 803 QYSNMCLSSFSALSWRSYKHTNSQFLYPADLVFNE 837
Db 561 QYSNMFLAVFALGWRSYROSSASLCLCFADLVINE 595

RESULT 12
GCR_SAGOE STANDARD: PRT: 777 AA.
ID GCR_SAGOE
AC P79269;
DT 01-NOV-1997 (Rel. 35, Created)

```

DT 01-NOV-1997 (Rel. 35, last sequence update)  
 DT 16-OCT-2001 (Rel. 40, last annotation update)  
 DE Glucocorticoid receptor (GR).  
 GN NR3C1 OR GR.  
 OS *Saguinus oedipus* (cotton-top tamarin).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 NC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saguinus.  
 NX NCBI\_TaxID=9490;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97176699; PubMed=9024238.  
 RA Reynolds P.D., Pittler S.J., Scammell J.G.:  
 RT "Cloning and expression of the glucocorticoid receptor from the  
 RT squirrel monkey (*Saimiri boliviensis boliviensis*), a glucocorticoid-  
 RT resistant primate".  
 RL J. Clin. Endocrinol. Metab. 82:465-472(1997).  
 CC -!- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN  
 CC THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR  
 CC PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES. BINDS TO THE  
 CC GRE TARGET SITE.  
 CC -!- SUBCELLULAR LOCATION: Nuclear.  
 CC -!- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,  
 CC A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.  
 CC -!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.  
 CC NR3 SUBFAMILY.  
 -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
 CC at the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 -----  
 DR EMBL: U87953; AAC51133.1; .  
 DR HSSP: P06536; IGDC.  
 DR InterPro: IPR001409; Glucocorticoid\_receptor.  
 DR InterPro: IPR000536; Hormone\_rec\_119.  
 DR InterPro: IPR001628; zf-C4.  
 DR Pfam: PF02155; GCR; 1.  
 DR Pfam: PF00104; hormone\_rec; 1.  
 DR Pfam: PF00105; zf-C4; 1.  
 DR PRINTS: PR00047; STEROIDRENGER.  
 DR SMART: SM00430; HOL1; 1.  
 DR SMART: SM00399; znf\_C4; 1.  
 DR PROSITE: PS00031; NOCLEAR\_RECEPTOR; 1.  
 DR Receptor; Transcription regulation; DNA-binding; Nuclear protein;  
 KW Zinc-finger; Steroid-binding.  
 MW 420  
 FT DOMAIN 1 420 NUCLEAR RECEPTOR-TYPE.  
 FT DNA\_BIND 421 486 C4-TYPE.  
 FT ZN\_FING 421 441 C4-TYPE.  
 FT ZN\_FING 457 481 HINGE.  
 FT DOMAIN 487 527 STEROID-BINDING.  
 FT DOMAIN 528 777  
 SEQUENCE 777 AA; 85593 MW; E4F9D24AEC5F9D58 CRC64;  
  
 Query Match 19.1%; Score 845; DB 1; Length 777;  
 Best Local Similarity 30.5%; Pred. No. 9.3e-38;  
 Matches 259; Conservative 103; Mismatches 227; Indels 260; Gaps 32;  
  
 QY 28 RSLSGTERDENNYM--ELVNVSCVSGAIPNNSTOGSSKEKELLPCCLOQDNNRGILT 85  
 DB 4 KESLTGPKKEPNSSVLTQEGNVMDCIKILRGATILKAVSYSSISLAQAQSDSKQORLLV 63  
 QY 86 SDIK---TELESKELSATVAESMGLYM---DSVRADADSYEQONQOGSKSPAKIYQNV 138  
 DB 64 DFKGVSNAQOPDLKSAVSLMGLVMGETETKVMGNDLGFPOGO----- 109  
 QY 139 QLVKFTKGNHRSSTLSCVTPPLRSPKSDSGSSVNGVMRAIYKSPIMCHEKSPSYCSPL 198  
 DB 110 -----ISLSGETDLDQ--LLESTIANLNI-----RSTSV--PE 137

QY 199 NMTSVCSFAGINSVSTTASTGSPFVHSPITQGTPLTCSFPAENNGSRSHSPAHASNV 258  
 DB 138 NPKSSASS-----SVSA----- 149  
 QY 259 SPLSPLSMKSSISPPSHCVKSPVSPNNVTLRSSVSPANINNSRCVSPSNTNN 318  
 DB 150 APREKEPKPHSHSVSEQQMLKQGTCTNCGNAKLCTADSTFDLIDLEFSSGSPKFTN 209  
 QY 319 RSTLSPFASTVGSICSPV--NNAFSTASTGSGASTLDVVP--SPDQEKGAQGVPP 375  
 DB 210 QSPWRSDLLIDENCLLSPLAGEBSFLLEGN--EDCKPLLPDK-----P 255  
 QY 376 KTEVESAISNGVTQQLNIVQYIKPEPDCAFSSSCGLGNSKINSDFSFPV--IKOSTKH 434  
 DB 256 KIKD-----NGDLVSSSNVTLPPQYKTEK--- 280  
 QY 435 SCSGTSFKNPYVNPFPFMDGSYFSEMDKDYISLGLIAPPPGPDGNCESGFFVGIK 494  
 DB 281 -----EDFTELC-----TPGV-----IK 293  
 QY 495 QEPDGSYPEASTPSSAIYG-----VNSGGSFHYRIGAOGTISLSRARDOS 543  
 DB 294 QE-KLSTVYCOASPPGANITGNKMSAISITGVSTSGGMHYDM-----NTASLSQ--QDOK 348  
 QY 544 FOHLSPFPVNTLVESW--KSHGD--LSSRRSDGYVPLEYIPENVSSTLR----- 590  
 DB 349 -PIRVVPIPIVGSENNRCOGSGDDMLTSLGTLPFGRTVFSNGYSPPMRDVSPPS 407  
 QY 591 SVSTGSS--RPSKILVGDASGCHGVVYVCGSKVFFKRAVGGHNYLACGRNDCTDK 649  
 DB 408 SSSVATGTPPKRLVCSDEASGCHGVVLTGSGKVFYKRAVEGHHNYLACGRNDCTDK 467  
 QY 650 IRRKNCPACRLQKLOAGMNLGARRSKRLGLKGIHEBQPOQOQPPPPPPSPBEGTT 709  
 DB 468 IRRKNCPACRYRKLQAGMNLGARRSK--KIKGI-----QOATT 505  
 QY 710 YIA-PAKPPSVNVLVPLSTISALPSPVMTVENIEPEIYVAGYDSSKPDPAENLST 768  
 DB 506 GVSQETSENPANKTIVP--ATLPQ-LTPVLVSLLEVEPLVGYSTVPDSTWRIMTT 562  
 QY 769 LNRLAGKQIQVWAKVLPFGKMLPLEDQTLTQYVMCLSSFALSRSYKHTNSOFLY 828  
 DB 563 LNMIGGROVIAVWAKAIPGFRNLHDDQMTLLQYVMPLMARALORSTRQASMLLC 622  
 QY 829 FAPDLVENE 837  
 DB 623 FAPDLTINE 631  
  
 RESULT 13  
 GCR\_MOUSE STANDARD; PRT; 783 AA.  
 ID GCR\_MOUSE 061628; 061629;  
 AC P06537; 061628 (Rel. 06, Created)  
 DT 01-JAN-1988 (Rel. 06, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Glucocorticoid receptor (GR).  
 GN NR3C1 OR GR OR GR1.  
 OS *Mus musculus* (Mouse).  
 NC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 NC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NX NCBI\_TaxID=10090;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87053816; PubMed=3780669;  
 RA Danielsen M., Northrop J.P., Ringold G.M.:  
 RT "The mouse glucocorticoid receptor: mapping of functional domains by  
 RT cloning, sequencing and expression of wild-type and mutant receptor  
 RT proteins".  
 RL EMBO J. 5:2513-2522(1986).  
 [2]  
 RP SEQUENCE OF 1-755 FROM N.A.  
 RX MEDLINE=89098404; PubMed=2911477;

RA Noho T., Kasai Y., Saito T.:  
 RT Novel CDNA sequence possibly generated by alternative splicing of a  
 RT mouse glucocorticoid receptor gene transcript from Shionogi carcinoma  
 RT 115.  
 RL Nucleic Acids Res. 17:445-445(1989).  
 CC -1- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN  
 CC THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR  
 CC PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES. BINDS TO THE  
 CC GRE TARGET SITE.  
 CC -1- SUBCELLULAR LOCATION: Nuclear.  
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A (SHOWN HERE) AND B; ARE  
 CC PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,  
 CC A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.  
 CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.  
 CC NR3 SUBFAMILY.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL: X04435; CAA28031.1; -  
 DR EMBL: X13358; CAA31738.1; -  
 DR EMBL: X13359; CAA31739.1; -  
 DR PIR: A25691; A25691.  
 DR HSSP: P06536; IGDC.  
 DR TRANSFAC: T00335; -  
 DR MGD: MGI:95824; NF3G1.  
 DR InterPro: IPR001409; Glucocrtcd\_receptor.  
 DR InterPro: IPR000536; Hormone\_rec\_1ig.  
 DR InterPro: IPR001628; zf-CA.  
 DR Pfam: PF02155; GCR: 1.  
 DR Pfam: PF00104; hormone\_rec: 1.  
 DR Pfam: PF00105; zf-CA; 1.  
 DR PRINTS: PR00047; STROIDPTNGER.  
 DR SMART: SM00430; HOL1; 1.  
 DR SMART: SM00399; znf-CA; 1.  
 DR PROSITE: PS00031; NUCLEAR RECEPTOR; 1.  
 KW Receptor; Transcription regulation; DNA-binding; Nuclear protein;  
 KW Zinc-finger; Steroid-binding; Alternative splicing.  
 FT DOMAIN 1 427 MODULATING.  
 FT DNA\_BIND 428 493 NUCLEAR RECEPTOR-TYPE.  
 FT ZN\_FING 428 448 CA-TYPE.  
 FT ZN\_FING 464 488 CA-TYPE.  
 FT DOMAIN 494 783 STEROID-BINDING.  
 FT DOMAIN 75 82 POLY-GLN.  
 FT VARSPLIC 458 458 G -> GR (IN ISOFORM B).  
 FT CONFLICT 437 437 V -> G (IN REF. 2).  
 FT SEQUENCE 783 AA; 86052 MW; 455E5C1C3C95F2A CRC64;  
 QY  
 Db 46 VANSVSGATPNNSTOGSSKEKQELLPC-----LODDNNRPGILTDITKELESKE 96  
 Db 40 VKVSSASSPSVA-AAQADSKQQRILDFSKGSASMAQQQQQQQP-----OPD 86  
 QY 97 LSATVAESMGLYV-----DSYRADYSEYDQNOQGSMPAKIYQVNEQVLYKNGNGHRPS 152  
 Db 87 LSKAVSLSMGLYGETETKVGNDLGYPOGGQLGSSGETDFRLLE-----133  
 QY 153 TISCVMTPLRSFMSDSSSSNGVMRAIVASPIIMCHEKSPVCSPLMTMTSSVSPAGINS 212  
 Db 134 -----SIANLNSTSRPE--NP 148  
 QY 213 VSTSTAFSGSFVHSPITGTGTLTCSNPAENRGRSHSPAHASVNGSPLSPLSMKSSI 272

Db 149 KSTTPAA-----GCATPTEKEFPQTHSDP-----SSEQONRKS-- 181  
 QY 273 SSPPSHCSVSPVSPNNVTLRSSVSSPANI--NNSRCSVSSPNTNRS-----T 321  
 Db 182 -----QPTNGGSAVKLYTTDQSTFDILQDLERSASGPKGETNESPMRSDLLIDEN 231  
 QY 322 LSSPAA-----SYVSGICSPVNNAFSTYASGTASGSLTDVYPPSPDTOKGAQEV 372  
 Db 232 LLSPLAGEDDFLELGDVNECKP-----LILPQTK-----262  
 QY 373 PEPTEVEASISNGVQGLNIVQYIKPEPDGARSSCLGNSKINSDFSPV--IKOES 431  
 Db 263 --PKIQDT-----GDTLSSPSSVALQVATEK 288  
 QY 432 TKHSCGTSFKGNFTVNPFPFMDGSYFEMDKDYSLSGILGPVCFDNCBGSFPV 491  
 Db 289 -----DFIELC-----TPGV-----299  
 QY 492 GIKQEPDGSYTPASIPSAIVG-----VNSGQSFHYRIGAGTISLSRSAR 540  
 Db 300 -IKQE-KLGPVYCOASFSGTNITIGNKMAISVHGVSSTSGGMVHYDM--NTASLSQO-Q 353  
 QY 541 DQSFQHLSSPPVYTVLIESMK-----SHGDIS--SRSDGPVLYEYIPENVS 585  
 Db 354 DQK-PVENVIPPIPVSGSENNMRGCGSEBDNLTSLGAMNFAGRSVFSGVSPGRPD--V 410  
 QY 586 SSTLRVSTGSSRPKICLYCGDEASGCHGVVTCGCKYEFKRAVSGQHNYLCAGRND 645  
 Db 411 SSPPSSSTATGPPKICLYCSDASVCHGVLTGCGCKYEFKRAVSGQHNYLCAGRND 470  
 QY 646 IIDKIRKNCBPACRLQCLQAGMNLGARKSKKLKLGHEBOPQOQPPPPPPPOSPE 705  
 Db 471 IIDKIRKNCBPACRYRKLQAGMNLGARKSK--KIRGIQDQATGAVSQ-----DTSE 520  
 QY 706 EGTIYIAPEKPSVNTALVQLSTISRALTPSPVAVLENEPELVAGYDSSKPDFAENL 765  
 Db 521 NAKNTIYPALPQ-----LPTLVSLLEVEPELVAGYDSSVDSASRI 565  
 QY 766 LSTNLRLAGKQIOVVMARVLPQFKNLPLEDQITLIQYSMCLSPALSRYKHTNSQ 825  
 Db 566 MTLNMLGGRQVIAVAKAIPGRFNLHLDQQTLLQYSWMLFADALGRSRYQASGN 625  
 QY 826 FLVPAADLVENE 837  
 Db 626 LICEFADPLINE 637  
 RESULT 14  
 ID GCR\_RAT STANDARD; PRT; 795 AA.  
 AC P06536; 008624;  
 DT 01-JAN-1988 (Rel. 06, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Glucocorticoid receptor (GR).  
 GN NR3C1 OR GR.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Hepaloma;  
 RX MEDLINE=86272086; PubMed=3755378;  
 RA Miesfeld R., Rusconi S., Godowski P.J., Mader B.A., Okret S.,  
 RA Wikstrom A.-C., Gustafsson J.-A., Yamamoto K.R.;  
 RT "Genetic complementation of a glucocorticoid receptor deficiency by  
 RL expression of cloned receptor cDNA";  
 RL Cell 46:389-399(1986).  
 RP (2)  
 RP SEQUENCE FROM N.A.  
 RA Heeley R.P., Gill E., van Zutphen B.;  
 RT "CAG repeat variation in the gene for rat glucocorticoid receptor";







```

AC 046567; 15-JUL-1999 (Rel. 38, Created)
BT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Glucocorticoid receptor (GR).
GN NR3C1 OR GR1.
OS Nairoli sciureus (Common squirrel monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.
OX NCBI_TaxID=9521;
RN [1]
RP SEQUENCE FROM N.A.
RA Patel P.D., Zhang Z., Ngo H., Lyons D.M., Schatzberg A.F.;
RT "Squirrel monkey (Saimiri sciureus) glucocorticoid receptor cDNA.";
RL Submitted (Jan-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Scammell J.G., Denny W.B., Valentine D.L.;
RT "Over-expression of the FK506-binding immunophilin Fkbp51 is the
common cause of glucocorticoid resistance in three neotropical
primates.";
RL Submitted (Jan-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN
CC THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR
CC PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES. BINDS TO THE
CC GRE TARGET SITE.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
CC A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
CC NR3 SUBFAMILY.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation - its
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
DR EMBL; AF041834; AAB97369.1; -
DR EMBL; AF337042; AAK01303.1; -
DR HSRP; P06536; IGDC.
DR InterPro; IPR001409; Glucocrtcd_receptor.
DR InterPro; IPR000536; Hormone_rec_1lg.
DR InterPro; IPR001628; zf-C4.
DR Pfam; PF02155; GCR; 1.
DR Pfam; PF00104; hormone_rec; 1.
DR PRINTS; PR00047; STEROIDFINGER.
DR SMART; SM00430; HOL1; 1.
DR SMART; SM00399; znf_C4; 1.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
KW Receptor; Transcription regulation; DNA-binding; Nuclear protein;
KW Zinc-finger; Steroid-binding.
FT DOMAIN 1 420 MODULATING.
FT DNA_BIND 421 486 NUCLEAR RECEPTOR-TYPE.
FT ZN_FING 421 441 C4-TYPE.
FT ZN_FING 451 481 C4-TYPE.
FT DOMAIN 487 527 HINE.
FT DOMAIN 528 778 STEROID-BINDING.
FT CONFLICT 498 498 MISSING (IN REF. 2).
SQ SEQUENCE 778 AA; 85738 MW; 721B8203939D1389 CRC64;

```

QY	86	SDIK----	TELESKE	LATVA	ENSG	GLYK----	DSVR	AD	AD	YS	EO	NO	GG	SM	SP	AK	TY	ONE	138											
Db	64	DFFPGSV	SN	AO	DP	LS	KA	VS	LS	MG	LT	GE	TE	TK	YMG	ND	GA	FP	OO	GI	SL	SG	GT	DI	OL	IE	123			
QY	139	OLYF	YK	GN	GH	RP	ET	LS	CV	NT	PL	RE	FM	DS	GS	SV	NG	VA	IV	KS	PI	MC	HE	KS	SP	VC	SP	198		
Db	124	EST-----																									129			
QY	199	NMT	SV	CS	P	AG	I	N	S	V	ST	TA	FS	GS	FP	YH	SP	IT	OG	ET	PL	TC	SP	NA	EN	K	S	258		
Db	130	NR	ST	VP	E----	NPK	S	S	A	S	S	V	S	A	A	P-----												160		
QY	259	SPL	S	PL	S	M	K	S	M	S	I	S	S	P	PH	S	V	A	P	S	P	N	N	T	L	R	S	317		
Db	161	SD	V	S	E	Q	ON	I	K	G	Q	G	Q-----															208		
QY	318	NR	ST	LS	FA	ST	AV	GS	I	CS	PV----	NNA	F	S	T	AS	T	AS	GS	ST	LD	VY	P-----	SP	TO	E	374			
Db	209	NQ	SP	M	K	S	D	L	L	D	EM	CL	S	P	L	A	G	E	D	S	F	L	E	GN	SN-----	ED	CK	254		
QY	375	P	K	T	E	V	E	S	A	I	S	NG	Y	T	G	O	L	I	N	I	O	Y	I	K	P	E	D	433		
Db	255	PK	I	X	O-----																							280		
QY	434	H	S	C	O	S	T	F	K	G	N	P	T	V	N	P	P	F	M	D	S	Y	F	E	M	D	K	Y	493	
Db	281	----																										292		
QY	494	K	O	E	P	D	D	S	Y	P	E	A	S	I	P	S	S	A	I	V	G-----								542	
Db	293	K	O	E	-----																							347		
QY	543	S	T	O	H	L	S	P	P	V	N	T	L	E	S	M-----													590	
Db	348	K	-----																									406		
QY	591	-SV	T	G	S	S-----	R	P	S	K	I	D	V	A	G	D	E	A	S	G	C	H	Y	V	T	G	S	C	648	
Db	407	S	S	S	S	T	A	T	T	G	P	P	K	L	C	V	O	S	D	E	A	S	G	C	H	Y	V	T	G	466
QY	649	K	I	R	R	K	N	C	P	A	C	L	O	K	L	O	A	G	M	I	G	A	R	K	S	K	L	K	I	708
Db	467	K	I	R	R	N	C	P	C	R	K	L	O	A	G	M	N	L	E	A	R	K	-----							505
QY	709	T	T	I	A	-----	P	A	K	S	P	N	T	L	I	P	O	L	I	S	T	A	L	I	P	S	P	A	V	767
Db	506	T	E	V	S	O	E	T	S	N	P	A	K	T	I	V-----														562
QY	768	T	N	R	L	A	G	K	O	M	I	O	V	K	A	V	L	P	G	F	K	M	L	P	E	D	O	T	I	827
Db	563	T	N	M	L	G	R	O	V	I	A	V	K	A	K	A	I	P	G	F	R	N	L							

Search completed: September 13, 2002, 10:21:51  
Job time: 290 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 13, 2002, 10:16:26 ; Search time 37.65 Seconds

(without alignments)  
3882.622 Million cell updates/sec

Title: US-09-695-293-42

Perfect score: 4422

Sequence: 1 METKGYHSLEPGIDMERMG.....FLYFAPDLVENELLARYREG 845

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL.19:\*  
1: sp.archaea:\*  
2: sp.bacteria:\*  
3: sp.fungi:\*  
4: sp.human:\*  
5: sp.invertebrate:\*  
6: sp.mammal:\*  
7: sp.mhc:\*  
8: sp.organelle:\*  
9: sp.phage:\*  
10: sp.plant:\*  
11: sp.podent:\*  
12: sp.virus:\*  
13: sp.vertebrate:\*  
14: sp\_virussified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4262	96.4	982	6	09N0W8
2	3515	79.5	706	4	096K09
3	807.5	18.3	732	13	09DDU9
4	787.5	17.8	438	6	0902M7
5	779.5	17.6	939	6	09GLEW0
6	764.5	17.3	583	13	09DEV4
7	756.5	17.1	710	13	09IBD5
8	754	17.1	853	13	093245
9	748.5	16.9	896	6	09GKI7
10	747	16.9	360	13	042274
11	745.5	16.9	359	13	091AC6
12	741.5	16.8	895	6	09GKN9
13	739	16.7	790	13	P70048
14	729.5	16.5	906	4	09UN21
15	727	16.4	848	13	09YGV9
16	724	16.4	797	13	09PMG5

17	719.5	16.3	769	13	093497	093497 pagrus major
18	716.5	16.2	401	13	0902M6	0902M6 petromyzon
19	714.5	16.2	563	13	09DDU4	09ddj4 halichoeres
20	709.5	16.0	854	13	093244	093244 oncorhynchus
21	708	16.0	730	4	013771	013771 homo sapien
22	669.5	15.1	303	6	097684	097684 ovis aries
23	644.5	14.6	344	13	091445	091445 serinus can
24	638.5	14.4	692	13	09W6F4	09w6f4 haplochromis
25	634.5	14.3	348	13	091425	091425 cnemidophor
26	602.5	13.6	284	13	090Y00	090y00 petromyzon
27	539.5	12.2	232	13	091A30	091a30 anolis caro
28	529	12.0	258	6	09BDJ7	09bdj7 ovis aries
29	495.5	11.2	298	6	09B547	09b547 ovis aries
30	486	11.0	200	13	0918F5	0918f5 pinepales
31	457.5	10.3	164	13	0902C2	0902c2 calotes ver
32	449.5	10.2	166	13	091698	091698 xenopus lae
33	446.5	10.1	554	13	0902M8	0902m8 petromyzon
34	434	9.8	553	13	090WS8	090ws8 brachydanto
35	429.5	9.7	431	6	0951I3	0951i3 ovis aries
36	422.5	9.6	153	11	0923G6	0923g6 mesocricetu
37	422	9.5	499	6	095MF0	095mf0 macaca arc
38	422	9.5	526	6	09BDM5	09bdm5 sus scrofa
39	420	9.5	553	13	098SM7	098sm7 brachydanto
40	414	9.4	569	13	098SM9	098sm9 brachydanto
41	412	9.3	564	13	090WV1	090wv1 carassius a
42	410.5	9.3	620	13	090WH6	090wh6 claritas gar
43	406.5	9.2	250	6	095JC0	095jc0 canis fami
44	401.5	9.1	592	13	090WS9	090ws9 brachydanto
45	400.5	9.1	486	6	095WE9	095we9 callithrix

## ALIGNMENTS

RESULT	ID	1	PRELIMINARY:	PRT:	982 AA.
09N0W8	AC	09N0W8			
DT	01-OCT-2000	(TREMBLrel. 15, Created)			
DT	01-OCT-2000	(TREMBLrel. 15, Last sequence update)			
DT	01-DEC-2001	(TREMBLrel. 19, Last annotation update)			
DE	MINERALOCORTICOID RECEPTOR.				
OS	Saimiri sciureus (Common squirrel monkey).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Saimiri.				
OX	NCBI_TaxID=9521;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Patel P.D.;				
RT	"Squirrel Monkey Mineralocorticoid Receptor cDNA.";				
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.				
CC	- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).				
CC	- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.				
DR	EMBL: AF245224; AAF63382.1; -.				
DR	HSSP: P06536; IRGD.				
DR	InterPro: IPR000536; Hormone_rec.119.				
DR	InterPro: IPR001723; Steroidhormone_receptor.				
DR	InterPro: IPR001628; zf-C4.				
DR	Pfam: PF00104; hormone_rec.1.				
DR	Pfam: PF00105; zf-C4; 1.				
DR	PRINTS: PR00398; STROHORMONER.				
DR	PRINTS: PR00047; STROIDFINGER.				
DR	SMART: SM00430; HOL1.1.				
DR	SMART: SM00399; zpf-C4; 1.				
DR	PROSITE: PS00031; NUCLEAR_RECEPTOR.1.				
KW	DNA-binding; Nuclear protein; Receptor; Transcription regulation;				
KW	zinc-finger.				
SO	SEQUENCE 982 AA; 107084 MW; E90C37E3302BC046 CRC64;				

Query Match 96.4%; Score 4262; DB 6; Length 982;  
Best Local Similarity 97.7%; Pred. No. 1.2e-279;  
Matches 818; Conservative 3; Mismatches 14; Indels 2; Gaps 2;

```
OY 1 METKGYHSLPGLDMERRMGVQSOAVERSSLGPTERTDENNYMEIYVSCVGAIPNNST 60
Db 1 METKGYHSLPGLDMERRMGVQSOAVERSSLGPTERTDENNYMEIYVSCVGAIPNNST 60
OY 61 QGSSKEKOEKLLPCLQODNNRPGILTSIDIKTELESKELSAIVAESMGLYMDSVRDADYSYE 120
Db 61 QGSSKEKOEKLLPCLQODNNRPGILTSIDIKTELESKELSAIVAESMGLYMDSVRDADY-YE 119
OY 121 QONOGSMSPAKIYQNWEOIYKFKNGHRPSTLSCVNTPLRSPMSDGSVNGVYARAI 180
Db 120 QONOGSMSPAKIYQNWEOIYKFKNGHRPSTLSCVNTPLRSPMSDGSVNGVYARAI 179
OY 181 VKSPTMCHKEKSPVCSPLMNTSSVCSFAGINSVSTTASFSGFPVHSPITQGTPLTCSPN 240
Db 180 VKSPTMCHKEKSPVCSPLMNTSSVCSFAGINSVSTTASFSGFPVHSPITQGTPLTCSPN 239
OY 241 AENRGRSHSPAHASNVGSPILSSPLSMKSSISPPSHCSVKSPVSPNNVTLRSSVSP 300
Db 240 VENRGRSHSPAHASNVGSPILSSPLSMKSSISPPSHCSVKSPVSPNNVTLRSSVSP 299
OY 301 ANINNSRCVSSPSTNNRSTLSSPAASTVGSICSPVNNAFSYTASGTSAGSSTLRDVP 360
Db 300 ANINNSRCVSSPSTNNRSTLSSPAASTVGSICSPVNNAFSYTASGTSAGSSTLRDVP 359
OY 361 SPDTQEKGAQOEVPFKTEVEESAINSGYTGOLNTYOYIKPEPDGAFSSCLGNSKIND 420
Db 360 SPDTQEKGAQOEVPFKTEVEESAINSGYTGOLNTYOYIKPEPDGAFSSCLGNSKIND 419
OY 421 SSFSPVTKOESTKHSCSGTSFSGKNPVNPFPMDGSYFSFMDKDYLSLGLIGPPVPGF 480
Db 420 SSFSPVTKOESTKHSCSGTSFSGKNPVNPFPMDGSYFSFMDKDYLSLGLIGPPVPGF 479
OY 481 DGNCEGSGPPVGIKQEPDDGSYTPPEASIPSSAIVGVNSGQSFHYRIGAOGTISLSRSAR 540
Db 480 DGNCEGSGPPVGIKQEPDDGSYTPPEASIPSSAIVGVNSGQSFHYRIGAOGTISLSRSAR 539
OY 541 DOSFOHLSFPVNTLVESKSHGDLSSRRSDGYVLEIYIPENVSSSTLRSTGSSRPS 600
Db 540 DOSFOHLSFPVNTLVESKSHGDLSSRRSDGYVLEIYIPENVSSSTLRSTGSSRPS 599
OY 601 KICLVGDEASGCHYGVTGCGSKVFFKRAVEGQHNLYLCAGRNDCLIDKIRKNCPCARL 660
Db 600 KICLVGDEASGCHYGVTGCGSKVFFKRAVEGQHNLYLCAGRNDCLIDKIRKNCPCARL 659
OY 661 QKCLQAGMNLGARKSKKLGKGIHBEROPOQOOPPPPPPOSPEGGTYIAPAKPSVN 720
Db 660 QKCLQAGMNLGARKSKKLGKGIHBEROPOQOOPPPPPPOSPEGGTYIAPAKPSVN 718
OY 721 TALVPOLSTISRALTPSPVAVLENIPEEIVYAGYDSKRPJAEMLLSTLNLRLAGKOMLOY 780
Db 719 TALVPOLSTISRALTPSPVAVLENIPEEIVYAGYDSKRPJAEMLLSTLNLRLAGKOMLOY 778
OY 781 VKNAKVLPGKRNLPLEQITLLIOYSWMCILSSPALSMSRYKHTNSOFLYFAPDLVFN 837
Db 779 VKNAKVLPGKRNLPLEQITLLIOYSWMCILSSPALSMSRYKHTNSOFLYFAPDLVFN 835
```

RESULT 2  
ID 096KQ9 PRELIMINARY; PRT; 706 AA.  
AC 096KQ9;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE MINERALOCORTICOID RECEPTOR DELTA.  
GN MR.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Plimates; Catarrhini; Hominiidae; Homo.  
OX NCBI\_TaxID=9606;  
GN [1]  
RP SEQUENCE FROM N.A.

```
FX MEDLINE-21410115; PubMed-11518808;  
RA Zennaro M.C., Souque A., Viengchareun S., Poisson E., Lombes M.;  
RT "A new human MR splice variant is a ligand-independent transactivator  
modulating corticosteroid action";  
RL Mol. Endocrinol. 15:1586-1598(2001).  
DR EMBL; AJ315514; CAC67405.1; -  
KW Receptor.  
SQ SEQUENCE 706 AA; 7506 MW; 03CF63D0ACEE981C CRC64;  
  
Query Match 79.5%; Score 3515; DB 4; Length 706;  
Best Local Similarity 99.4%; Pred. No. 2,4e-229;  
Matches 670; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
  
OY 1 METKGYHSLPGLDMERRMGVQSOAVERSSLGPTERTDENNYMEIYVSCVGAIPNNST 60  
Db 1 METKGYHSLPGLDMERRMGVQSOAVERSSLGPTERTDENNYMEIYVSCVGAIPNNST 60  
OY 61 QGSSKEKOEKLLPCLQODNNRPGILTSIDIKTELESKELSAIVAESMGLYMDSVRDADYSYE 120  
Db 61 QGSSKEKOEKLLPCLQODNNRPGILTSIDIKTELESKELSAIVAESMGLYMDSVRDADYSYE 120  
OY 121 QONOGSMSPAKIYQNWEOIYKFKNGHRPSTLSCVNTPLRSPMSDGSVNGVYARAI 180  
Db 121 QONOGSMSPAKIYQNWEOIYKFKNGHRPSTLSCVNTPLRSPMSDGSVNGVYARAI 180  
OY 181 VKSPTMCHKEKSPVCSPLMNTSSVCSFAGINSVSTTASFSGFPVHSPITQGTPLTCSPN 240  
Db 180 VKSPTMCHKEKSPVCSPLMNTSSVCSFAGINSVSTTASFSGFPVHSPITQGTPLTCSPN 240  
OY 241 AENRGRSHSPAHASNVGSPILSSPLSMKSSISPPSHCSVKSPVSPNNVTLRSSVSP 300  
Db 240 VENRGRSHSPAHASNVGSPILSSPLSMKSSISPPSHCSVKSPVSPNNVTLRSSVSP 300  
OY 301 ANINNSRCVSSPSTNNRSTLSSPAASTVGSICSPVNNAFSYTASGTSAGSSTLRDVP 360  
Db 301 ANINNSRCVSSPSTNNRSTLSSPAASTVGSICSPVNNAFSYTASGTSAGSSTLRDVP 360  
OY 361 SPDTQEKGAQOEVPFKTEVEESAINSGYTGOLNTYOYIKPEPDGAFSSCLGNSKIND 420  
Db 360 SPDTQEKGAQOEVPFKTEVEESAINSGYTGOLNTYOYIKPEPDGAFSSCLGNSKIND 420  
OY 421 SSFSPVTKOESTKHSCSGTSFSGKNPVNPFPMDGSYFSFMDKDYLSLGLIGPPVPGF 480  
Db 421 SSFSPVTKOESTKHSCSGTSFSGKNPVNPFPMDGSYFSFMDKDYLSLGLIGPPVPGF 480  
OY 481 DGNCEGSGPPVGIKQEPDDGSYTPPEASIPSSAIVGVNSGQSFHYRIGAOGTISLSRSAR 540  
Db 481 DGNCEGSGPPVGIKQEPDDGSYTPPEASIPSSAIVGVNSGQSFHYRIGAOGTISLSRSAR 540  
OY 541 DOSFOHLSFPVNTLVESKSHGDLSSRRSDGYVLEIYIPENVSSSTLRSTGSSRPS 600  
Db 541 DOSFOHLSFPVNTLVESKSHGDLSSRRSDGYVLEIYIPENVSSSTLRSTGSSRPS 600  
OY 601 KICLVGDEASGCHYGVTGCGSKVFFKRAVEGQHNLYLCAGRNDCLIDKIRKNCPCARL 660  
Db 601 KICLVGDEASGCHYGVTGCGSKVFFKRAVEGQHNLYLCAGRNDCLIDKIRKNCPCARL 660  
OY 661 QKCLQAGMNLGARK 674  
Db 661 QKCLQAGMNLGERR 674
```

RESULT 3  
ID 09DDU9 PRELIMINARY; PRT; 732 AA.  
AC 09DDU9;  
DT 01-MAR-2001 (TREMBLrel. 16, Created)  
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE PROGESTERONE RECEPTOR.  
GN XPR-1.  
OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OK NCBI\_TaxID=8355;  
 RN  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=20570484; PubMed=11114187;  
 RX Tian J., Kim S., Heilig E., Ruderman J.V.;  
 RT "Identification of XPR-1, a progesterone receptor required for Xenopus  
 RT oocyte activation.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 97:14358-14363(2000).  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.  
 DR EMBL: AF279335; AAG42362.1; -.  
 DR HSSP: P06536; IRGD.  
 DR InterPro: IPR000536; Hormone\_rec\_1lg.  
 DR InterPro: IPR001128; Progesterone\_receptor.  
 DR InterPro: IPR001628; Steroidhormone\_receptor.  
 DR Pfam: PF00104; hormone\_rec.1.  
 DR Pfam: PF02161; Prog\_receptor.1.  
 DR Pfam: PF00105; zf-C4.1.  
 DR PRINTS: PR00398; STRDHOMER.  
 DR PRINTS: PR00047; STROIDFINGER.  
 DR SMART: SM00430; HOLI.1.  
 DR SMART: SM00399; ZnF\_C4.1.  
 DR PROSITE: PS00031; NUCLEAR\_RECEPTOR.1.  
 KW DNA-binding; Nuclear protein; Receptor; Transcription regulation;  
 KW Zinc-finger.  
 SQ SEQUENCE 732 AA; 82022 MW; BFOBA3A1AF022199 CRC64;

Query Match 18.3%; Score 807.5; DB 13; Length 732;  
 Best Local Similarity 31.3%; Pred. No. 2.6e-46;  
 Matches 232; Conservative 94; Mismatches 194; Indels 221; Gaps 31;  
 QY 133 IVONVQLVKFYKNGHNRSTLSCVNTPLRSFMSDGSVNGVMRAIKYSPIMCEKSP 192  
 DB 30 LVOREPHEGSIYKKGEG--PSS-----PDNNLDEN--VLDSIIDS----- 64  
 QY 193 SVCSPLNMTSVYCSVSPAGINVSSTTASFGSPFVHSPITQGTPLTCSPAENRGRSHSPA 252  
 DB 65 -----SSASSHLHSMWHFAA--PEVSRVTPTMHC--PDEAKALSH----- 101  
 QY 253 HASNVGSLPSPLSKSKSISSPPSHCSYKSPVSSPNNVTLRSSVSSPANINNSRCSVSS 312  
 DB 102 HTS-----SLEETSLMAAPTLVERKEP-----GDSMPYKGGKSLSEETKE 140  
 QY 313 PSNTNNRSTLSSPAASTVSGISCS-----PVNNAF-----SYTASGTGAGSS 353  
 DB 141 PN-----SSLTMDSDETVTSILPLPPLDNLNMPILPLNPAVLAVARAOILGEGEGOR 195  
 QY 354 TLRDVPSPDPTQEKGAQVFPPTKTEVEESAISNGVYQOLNIQYIKPEPDGAFFSSCLG 413  
 DB 196 S-----SPDTQ-----TSTPYANLQ-----NMKQISYFPDPQDP----- 228  
 QY 414 NSKINSDFSFPVTKOESTKHSCTSEKGNP-----TVNPFPPMDGSIYSPMDK--DY 467  
 DB 229 --RIKKES--TVSLYKAAKESSTLGQDYGSSPQNPSTPDPSL--NFLYKNDASCDYD 283  
 QY 468 SLGLIGPPVPGFDNCGEGSGFPVGIKQEPDDGSYVPEASISATVGNSSGQSHYRI 527  
 DB 284 SK-----ISTGNTSBSG-----CVLPST-----AQTIYQPL 312  
 QY 528 GAQGTLSLSRSARDQSFQHLSSFPVNTLVESMKSHGDL--SSRRSDGYPVLEYIPENV 584  
 DB 313 SLNG-----HQHI--TFQP--TSMKETLYLSEIQLPYVYIRSDNP----- 349  
 QY 585 SSSLRSVSTGS-----SRPKICLVCGDEASGCHGVVTCGSCKVFRRAYEGQHNYLC 639  
 DB 350 -----DGPSPFSEFTFPQKICILCGDEASGCHGVVTCGSCKVFRRAYEGQHNYLC 401  
 QY 640 AGRNDCIIDKIRKNCOPACRLQCLQAGMNLGARKSKKLGKLGHEBQPOQOQPPPPPP 699

DB 402 AGRNDCIIVDKIRKNCOPACRLQCCQAGVYLGGRKRRKGRITGHEIDVTYVQSP----- 457  
 QY 700 PROSPEEGTITYIAPAKEPSVNTALVPOLSTISR--ALTPSPVMELENIEPELVAGTOS 756  
 DB 458 -----PTLSLRCOOILIRRISSNSAQEIQFTPELLQILQSIIEPEVYVAGYDN 504  
 QY 757 SKPDTAENLSTLNRLAGKOMIOVVKARVLPFKRLPLEDOTTLTOYSGMCCSLFSALM 816  
 DB 505 TQEPFSTALLSLNQCEKQVLCVVKWSKSLPGRNLHIDDTLLQYSMSMLMVEFALGM 564  
 QY 817 RSYKHTNSOFLYFAPDLVFN 837  
 DB 565 RSYQHYSGQMLFAPDLVFN 585  
 RESULT 4  
 ID 0902M7 PRELIMINARY: PRT: 438 AA.  
 AC 0902M7;  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)  
 DE CORTICOID RECEPTOR (FRAGMENT).  
 OS Petromyzon marinus (Sea lamprey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;  
 OC Petromyzontiformes; Petromyzontidae; Petromyzon.  
 OK NCBI\_TaxID=7757;  
 RN  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21244662; PubMed=11331759;  
 RA Thornton J.W.;  
 RT "Evolution of vertebrate steroid receptors from an ancestral estrogen  
 RT receptor by ligand exploitation and serial genome expansions.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:5671-5676(2001).  
 DR EMBL: AY028457; AAK20930.1; -.  
 KW Receptor.  
 FT NON-TER 1 1  
 SQ SEQUENCE 438 AA; 48935 MW; B86FEE6637BF471 CRC64;  
 Query Match 17.8%; Score 787.5; DB 13; Length 438;  
 Best Local Similarity 49.8%; Pred. No. 3e-45;  
 Matches 161; Conservative 40; Mismatches 85; Indels 37; Gaps 6;  
 QY 520 GSFHYRIGAOGTISLSRSARDQSFQHLSSFPVNTLVESMKSHGDLSSR--RSDGYPVY 577  
 DB 1 GVEFQLPYASAT--SPRPVATSSAGISINFSNGN-----NFGPLSPNGVQGDGFPYP 52  
 QY 578 EYIPEVSSSTLRSVSTGSSRPSKICLVCGDEASGCHGVVTCGSCKVFRRAYEGQHNY 637  
 DB 53 GF-----TSPQASSVPQKACILCSDEASGCHGVVTCGSCKVFRRAYEGQHNY 102  
 QY 638 ICAGRNDCIIDKIRKNCOPACRLQCLQAGMNLGARKSKKLGKLGHEBQPOQOQPPPP 697  
 DB 103 ICAGRNDCIIDKIRKNCOPACRLQCLQAGMNLGARKSKKLGKLGHEBQPOQOQPPPP 697  
 QY 698 PPPQSPPEEGTITYIAPAKEPSVNTALVPOLSS--TISRALTSPSPVNLNIEPEIYAGY 754  
 DB 163 SATPO-----SSNSTAVTTFSPPTGEPJFSPPLMILQIAIEPEVVMG 208  
 QY 755 DSKPDTAENLSTLNRLAGKOMIOVVKARVLPFKRLPLEDOTTLTOYSGMCCSLFSAL 814  
 DB 209 DNTRSQTTAYMSSLNRLCDKOLVSYVKAWSKSLPGRNLHIDDTLLQYSMSMLMVEFAL 268  
 QY 815 SMRSYKHTNSOFLYFAPDLVFN 837  
 DB 269 SMRSYKHTNSOFLYFAPDLVFN 291  
 RESULT 5  
 ID 09GLM0 PRELIMINARY: PRT: 939 AA.

```

AC O9ELW0;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE PROGESTERONE RECEPTOR.
GN PR.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Lantinga-van Leeuwen I.S., van Garderen E., Mol J.A.;
RT "Molecular cloning and cellular localization of the canine
  progesterone receptor.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
DR EMBL; AF177470; AAG09282.1; -.
DR HSSP; P06401; 1A28.
DR InterPro; IPR000536; Hormone_rec_1lg.
DR InterPro; IPR000128; Progesterone_receptor.
DR InterPro; IPR001723; Sterdihormone_receptor.
DR InterPro; IPR001628; zf-C4.
DR Pfam; PF00104; hormone_rec.1.
DR Pfam; PF02161; Prog_receptor.1.
DR PRINTS; PR00105; zf-C4; 1.
DR PRINTS; PR00398; STRDHOMONER.
DR PRINTS; PR00047; STROIDFINGER.
DR SMART; SM00430; HOL1; 1.
DR SMART; SM00399; znf_C4; 1.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
DR DNA-binding; Nuclear protein; Receptor; Transcription regulation;
  zinc-finger.
KW SEQUENCE
SQ
Query Match 17.6%; Score 779.5; DB 6; Length 939;
Best Local Similarity 30.9%; Pred. No. 2.9e-44;
Matches 217; Conservative 97; Mismatches 246; Indels 143; Gaps 23;
OY 188 HEKSPVCSPPLMNTSSVCS-----PAGINSVSTTASF-----GSEPVH---SPITRGTP 234
DB 192 HKCPFGSLPSRQPLPLCPGAMHPGAAKATQPALGVDEGCPAAGSGPILTKGP 251
OY 235 LTCSPAENKGRSHSPAHASVNSPL---SSPLSMKSISPSPHCVKSPVSSPNV 291
DB 252 RPPAGPAAAAAGAPAPGTAAPGTAPVPKEDSRTPAPKGSLEQ---DAPAPGCSPLAT 307
OY 292 TLKSSVSSP-----ANINNSRCVSSPSMNTNNSSTLSSPAASTVSGISPVNNAFSTAS 346
DB 308 TMDQFTHVPLPLGSAFLAKRTQLLEATETYGDAAPRRGSP-SAPCAPL-----AA 359
OY 347 GTSAGSSTLADVVPSPDTEKGAQVEFPKTEVESAIISNGVTGOLINVOYIKPEPDGAF 406
DB 360 GDEPDCAVPSDAPPKDA-----FLYGDFOQPALK-----IKEEGEAB 399
OY 407 SSS-----CLGNSKINSDFSVPKQESTKHSCSGTFKGNPTV----- 447
DB 400 AARSPPRYLAAGPHSCVFAADAPPALPALPLPRLPRASSRPGGAPAAAAACGSSAS 459
OY 448 NPPPFMDGSEYFSPMDKDYSLSGILGPPVPGFGDNGCEGSGFVGIKQEPDDGSSYPEAS 507
DB 460 SPQPALECV-----LYKAGAPPPPOGPFMAAPCRVPG--AGACILPRDCA-----AA 504
OY 508 IPSAIVGVNSG-----GQSFHYRIGAQGTISLSRSARDQSEFOHLSFPPVNTLVESMKS 562
DB 505 AASAGAGASPALYQPLGLALPOLGYOAAV--LKEGLPQVYO----- 545
OY 563 HGLDSKRSRGYPVLEYIIPENVSSSTLRASVSTGSSRPSKICLVCGDEASCHGYVTCGS 622
DB 546 -----PYLNLRLPDSDSASQSPQYSF--ESLPQKICLIGDEBASCHGYVITCGS 592

```

```

OY 623 CKVEFRAYEGOHNYLCAGRNDCTIDKIRKKNCPACRLQCLQAGMNLGARRSKLGLK 682
DB 593 CKVEFRAYEGOHNYLCAGRNDCTIDKIRKKNCPACRLKCCQAGMVLGRRKFKFNVR 652
OY 683 GIHE-EGPQOQOPPPPPPPSPPECTYIAPAKEPSVFALVPOLSTISRALTFSPKVY 741
DB 653 VMRTLDAVALPQGVGIPNESQALSQRISF-----SPSODIOLIPPL-----INTL 696
OY 742 LEMIEPIYVAGDSSCKPTAEMLSTLNRLAGKQMIQVAKVLPGRKNLPLEQITL 801
DB 697 LMSIEPVYIAGHDNTRKPTDSSSLTSLNOLGERQLSTVYKSKSLPGFRNHIDQITL 756
OY 802 IOYSMCLSSFALSWRSYKHTNSQPLFPADVLVENELLARVR 844
DB 757 IOYSMCLSWLFGWRSYKHSYQMLYFADLILNE--QRMK 797
RESULT 6
O9DEV4 PRELIMINARY; PRT; 583 AA.
O9DEV4
AC O9DEV4;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE PROGESTERONE RECEPTOR PR.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-20524048; PubMed-11050156;
RA Bayra M., Booth R.A., Sheng Y., Liu X.J.;
RT "The classical progesterone receptor mediates Xenopus oocyte
  maturation through a nongenomic mechanism.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:12607-12612(2000).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
DR EMBL; AY007198; AAG01366.1; -.
DR HSSP; P06536; 1RGD.
DR InterPro; IPR000536; Hormone_rec_1lg.
DR InterPro; IPR000128; Progesterone_receptor.
DR InterPro; IPR001723; Sterdihormone_receptor.
DR InterPro; IPR001628; zf-C4.
DR Pfam; PF00104; hormone_rec.1.
DR Pfam; PF02161; Prog_receptor.2.
DR PRINTS; PR00398; STRDHOMONER.
DR PRINTS; PR00047; STROIDFINGER.
DR SMART; SM00430; HOL1; 1.
DR SMART; SM00399; znf_C4; 1.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
DR DNA-binding; Nuclear protein; Receptor; Transcription regulation;
  zinc-finger.
KW SEQUENCE
SQ
Query Match 17.3%; Score 764.5; DB 13; Length 583;
Best Local Similarity 37.9%; Pred. No. 1.6e-43;
Matches 185; Conservative 56; Mismatches 134; Indels 113; Gaps 16;
OY 361 SPDTQEKGAQVEFPKTEVESAIISNGVTGOLINVOYIKPE--PDGARSSSCGLGNSKIN 418
DB 51 SPDTSQ---TSVPFNLPNNVKQIS-----YFNPEIQDP-----PRIK 85
OY 419 SSS-----ESVPIKQESTHSCSGTSFKNPTVNPFPMDGSEYFSPMDKDYSLSGITL 474
DB 86 KDSISVILTKVAK--ESTLCQDYGSSPRNPSTPDPDPSLDFLYK--NNDYOCFKS----- 139
OY 475 PVVPGFDNGCEGSGFPVGIKQEPDDGSSYYPEASIVGVNSGGQSFHYRIGAQG--T 532
DB 140 -----HGN-----TNEGCGCLIPSTYS-----AQTIYQPLSLNGHOY 170

```

```

QY 533 ISLSRARDQSFOHLSFPFVNTLVESKSHGDLSSRRSDGYPVLEYIPEVSSSTLRSV 592
DB 171 VTPQPTMKETVLPQIOLPVTYI-----RSDGDE-RCIPFSF----- 208
QY 593 STGSSRSKICLVGDASGCHGVVTCGSKVEFKRAVEGOHNYLCAGNDCTIDKIRR 652
DB 209 ---EMLPQKICICGDASGCHGVLTGCGSKVEFKRAIEGHONYLCAGNDCTVDKIRR 265
QY 653 KNCPCRLQKCLQAGMNLGARKSKLGLKGIHEEQPOQOOPPPPPQSPBEGTYIA 712
DB 266 KNCPCRLQKCLQAGMNLGARKSKLGLKGIHEEQPOQOOPPPPPQSPBEGTYIA 308
QY 713 PAKEPSVNTLVAPOLSTISR---ALTPSPVMEVNIPEPELVAGYDSSKPDFAENLLSTL 769
DB 309 PTLSECCQILIRISNSSAOEIQFPELLQILQSTIEPEVYAGYDTQEPSPALLSTL 368
QY 770 NTLAGKOMIOWVAKVLPFGKNLPLEDQITLQYSWMCSSPALSWSRYKHTNSQFLYE 829
DB 369 NOLCEBRLQVGVKSKSLPFRNLHIDDQITLQYSWMSLWVFLGMSYQHSQGMLYF 428
QY 830 APDLVENE 837
DB 429 APDLVENE 436

```

```

RESULT 7
Q91BD5 PRELIMINARY; PRT; 710 AA.
AC Q91BD5;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
DE PROGESTERONE RECEPTOR.
GN PR.
OS Anguilla japonica (Japanese eel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;
OC Anguillidae; Anguilla.
OX NCBI_TaxId=937;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RX MEDLINE=20088790; PubMed=10620698;
RA Todo T., Ikeuchi T., Kobayashi T., Kajiwara-Kobayashi H., Suzuki K.,
RA Yoshikuni M., Yamauchi K., Nagahama Y.;
RT Characterization of a testicular 17,20-dihydroxy-4-pregnen-3-one (a
RT spermatation-inducing steroid in fish) receptor from a teleost,
RT Japanese eel (Anguilla japonica).";
RL FEBS Lett. 465:12-17(2000).
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
DB EMBL; AB032075; BAA89539.1; -.
DR HSSP; P06536; IRGD.
DR InterPro; IPR000536; Hormone_rec_11g.
DR InterPro; IPR001723; Steroidhormone_receptor.
DR InterPro; IPR001628; zf-C4.
DR Pfam; PF00104; hormone_rec; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PRO0398; STRODHORMNER.
DR PRINTS; PRO0047; STROIDFORMER.
DR SMART; SM00430; HOLI; 1.
DR SMART; SM00399; ZNF_C4; 1.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
KW Zinc-binding; Nuclear protein; Receptor; Transcription regulation;
KW Zinc-finger.
SQ SEQUENCE 710 AA; 78819 MW; 0C8149B05CA055AA CRC64;

```

Query Match 17.1%; Score 756.5; DB 13; Length 710;  
 Best Local Similarity 31.4%; Pred. No. 7.1e-43;  
 Matches 210; Conservative 84; Mismatches 192; Indels 183; Gaps 20;

```

QY 233 TPLTSPNAENRGRSRSHPAHASNVGSPLSPLSSMKSSISPPSHCSVKSVPVSNVNT 292
DB 14 TPARASFPD-----ASTIRARNLKITYESGSIYEELVRDS-----NNIQ 57
QY 293 LRSSV-----SSPANINNSRCSVSSPSNTRSTLSPAATVG-SLCSPVNNAFSYTAG 347
DB 58 SLSSVPLPLMNFQMDLTLCAPGSGSDSELMKDEYVGVGNSVSKDTCGHE-ISTAE 115
QY 348 TSAGSSTLRDVVSPDTPQEGAOEVPPTKEVEBSAISN-----GVTGQINYOYIKPEP 402
DB 116 LSWMAAPL-----SREETLQAGTVVPAVTPKESEFATSNFSASGISIKDEOOSLMEP 171
QY 403 DGA-----FSSCLGNSKINSDFSFPDIXQ---ESTKHS---C 436
DB 172 QSSDFCPYTNIRKLPSTYLTNTASTKQLGIDGQDPTSAHSSPPAQKIVLDIARTASDL 231
QY 437 S-----GTSFKGNPTVNPFPMDGSYFSPMDKDYSLSGIIGPVPFGDNC----- 484
DB 232 SDNPLPQATNLIKTDPC-----SSFSFVGE-----GILTRASMGYSQAQIOTLPV 276
QY 485 -EGSGFPVGIKQEPDGSYTPKASIPSSAIVGVNSGOSFHYRIGAGCTISLSRARDQS 543
DB 277 HKSEPFRLSASAPADSPFCQSTGSPS-----EDHNLQIDYLSAPGLHSTCKYSS 326
QY 544 FOHLSFPVNTLVESKSHGDLSSRRSDGYPVLEYIPEVSSSTLRSVSTGSSRPSKIC 603
DB 327 TNAYSTLVG-----LPQVC 342
QY 604 LVCGDEASGCHGVVTCGSKVEFKRAVEGOHNYLCAGNDCTIDKIRKNCPCRLQK 663
DB 343 VICGDASGCHGVLTGCGSKVEFKRAVEGHNNYLCAGNDCTIDKIRKNCPCRLQK 402
QY 664 LQAGMNLGARKSKLGLKGIHEEQPOQOOPPPPPQSPBEGTYIAPAKESVNTAL 723
DB 403 YQAGMILGGRKLLKGLAKA-----AGLTQALVASHL 434
QY 724 VP-OLSTISRALP-----SP---VMYLENIEPELVAGYDSSKPDFAENLLST 768
DB 435 TPKRLSGDSOLAMPUGCLPGVRELHLSPOITVLESIEPEVYAGYDSSKPDFAENLLST 494
QY 769 LNRLAGKOMIOWVAKVLPFGKNLPLEDQITLQYSWMCSSPALSWSRYKHTNSQFLYE 828
DB 495 LNRLCEQLRLRYKWSKSLPGRSLHINDQMALQYSWMSLWVFLGMSYQHSQGMLYF 554
QY 829 FAPDLVENE 837
DB 555 FAPDLVENE 563

```

```

RESULT 8
Q93245 PRELIMINARY; PRT; 853 AA.
AC Q93245;
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
DE ANDROGEN RECEPTOR BETA.
GN AR-BETA.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxId=8022;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99150354; PubMed=10026186;
RA Takeo J., Yamashita S.;
RT "Two distinct isoforms of cDNA encoding rainbow trout androgen
RT receptors."
RL J. Biol. Chem. 274:5674-5680(1999).
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
DB EMBL; AB012096; BAA32785.1; -.

```

DR HSSP; P06536; 1GDC.  
 DR InterPro; IPR001103; Androgen\_recep.  
 DR InterPro; IPR000536; Hormone\_rec\_119.  
 DR InterPro; IPR001628; zf-C4.  
 DR Pfam; PF02166; Androgen\_recep. 1.  
 DR Pfam; PF00104; hormone\_rec. 1.  
 DR Pfam; PF00105; zf-C4; 1.  
 DR PRINTS; PR0047; STROIDINGER.  
 DR SMART; SM00430; HOL1; 1.  
 DR SMART; SM00399; ZnF\_C4; 1.  
 DR PROSITE; PS00031; NUCLEAR\_RECEPTOR; 1.  
 DR DNA-binding; Nuclear protein; Receptor; Transcription regulation;  
 KW Zinc-finger. 853 AA; 95776 MW; 65EFF5PD3B36f4C4 CRC64;  
 SQ

Query Match 17.1%; Score 754; DB 13; Length 853;  
 Best Local Similarity 27.3%; Pred. No. 1,3e-42;  
 Matches 241; Conservative 125; Mismatches 285; Indels 232; Gaps 33;

QY 9 LPEGLDMERRRGOVSQAVERSLSGPTERTDENNYMEIVNVCYSGAIPNNST-----Q 61  
 DB 3 IPVGL-----GGVCDSPNIVFRGPQNVFHN-----YKATLPNTVTETLDFS 46  
 QY 62 GSKEKEQELLPCLOQDNNRGLITSDIKTELESKELSATVAESMGLYMDSVRADVSYEQ 121  
 DB 47 SSYFNMQNHPEMRQJNR-----QSPKEIISGTA-----RNSDIEVKE 86  
 QY 122 QNCGGSPAKIYQNEQOLYKFKNGHPSLSCVNTPLRSPMSDGGSGVNGVNAIY 181  
 DB 87 DD---SISFRTLESADARRHFASKSGNKTFGSVNELDYPNANGYSGDRP----- 136  
 QY 182 KSPIMCHEKSPVSCSP-----LNMITSVCSPAGITSVSTASFCSEFVHSP 228  
 DB 137 --PLACNTKC-QCCQPVPHHVELSPNSYARVANCSNACTTIISETARE-----LCA 188  
 QY 229 ITGCTPLTSPNANENGRSHSPAHASNVGSPPLSSPKSSISSPSHCSYKSPVSSP 288  
 DB 189 VSVSLGTLMLNEMNDIGPYNAASSAND-----QSGCNLYLFQVPLNCS-----GAE 235  
 QY 289 NNYTLRVSVPANINNSRCSVSSPNTNRSSTLSSFASTVSGICSPVNAFSTYASGT 348  
 DB 236 ENV-----STREYKC-----PSEARNARPLQSDTRVAMFKS--SPANDLIEEVA 279  
 QY 349 SAGSSTLRDVVPSPDQF-KGAQEVPPPKKEEYESAISNVTG-----QLNIQYI 398  
 DB 280 HLSSRH-----PSTGEDEFRLNEKSDDPISKETENSLSTARASCHFDLPLAHLAHS 334  
 QY 399 KPEPDGAFS-----SSCLGNSKINS-----DSFSVPIKQESTKHSCGTSFGKNP 448  
 DB 335 QTDPRISSHVIAHVCEGTETMEDKADYDLOOQYSVKIYEALISNEPACTSW----- 387  
 QY 449 PEPMDGSYSFEMDDKYIYLSLGLPVPVGFQDNGSGSGFPVGIKQEPDGSYTPASI 508  
 DB 388 -----SSQYV-----GYNDN-----DNTQYGPQGM 408  
 QY 509 -PSSAIVGVNSG--GQSFHYRIGAQTITLSRSARDOSF-----OHLSSFPVNTLVE 558  
 DB 409 NPYSR--GPDGFTICNPYEYERKG-GLVRRRPISSEOWYEGGMGRPYNSPLTKMEVG 465  
 QY 559 SWKSHGDLSSRRSG-----YVLEYIPENVSSSTLRSVSTGSSPSKICLVCGDEASGCH 614  
 DB 466 DMLVSYTDAFEGGRDHMPMEFFFP-----PQRTCLICADAEASGCH 508  
 QY 615 YGVATGSCCKYFKRAVEGHNITACAGNCTIDKIRKKNOPARLOKIOAGNGLGARK 674  
 DB 509 YGALTGSCCKYFKRAVEGHNITACAGNCTIDKIRKKNOPARLOKIOAGNGLGARK 568  
 QY 675 SKKLGKLGKIEEQPOQOQPPPPPPQSPPEEGTYYIAPAKPEPVNTALVOLPSTISRAL 734  
 DB 569 LKRTGQLKSPEDLP--TQGTDAIQCVSPSGLTFHS-----QLVELN--- 610  
 QY 735 TPSPVAVLENTIEPIYAGYDSSKPDTAENLSTLNRLAKQKIQVYKMAKVLPGFKNLP 794

DB 611 -----LIESIEPYNVAGHDCQPDSSAAVLTLSLNLGEKOLYKVKMAKMGFRNLH 664  
 QY 795 LEDDTILQYWMKLSFALSMSRKYHTNSQFLYFAPDLVENE 837  
 DB 665 VDDQVTVIQHSWMGMVFGIGLRSYKNVNAKMLYFADPLVEND 707

RESULT 9  
 Q9GKL7 ID Q9GKL7 PRELIMINARY; PRT; 896 AA.  
 AC Q9GKL7;  
 DT 01-MAR-2001 (Tremblrel, 16, Created)  
 DT 01-MAR-2001 (Tremblrel, 16, Last sequence update)  
 DT 01-DEC-2001 (Tremblrel, 19, Last annotation update)  
 DE ANDROGEN RECEPTOR.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=PIUTITARY;  
 RA Song J.H., Fahrenkrug S.C., Rohrer G.A., Wise T.H., Ford J.J.;  
 RT "Porcine androgen receptor (AR) cDNA cloning: Expression in pituitary associates with FSH secretion in boars."  
 RL Submitted (NOV-1999) to the EMBL/Genbank/DBJ databases.  
 CC 1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
 CC 1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.  
 DR EMBL; AF202775; AAG37994.1; -.  
 DR HSSP; P06536; 1GDC.  
 DR InterPro; IPR001103; Androgen\_recep.  
 DR InterPro; IPR000536; Hormone\_rec\_119.  
 DR InterPro; IPR001628; zf-C4.  
 DR Pfam; PF02166; Androgen\_recep. 1.  
 DR Pfam; PF00104; hormone\_rec. 1.  
 DR PRINTS; PR0047; STROIDINGER.  
 DR SMART; SM00430; HOL1; 1.  
 DR SMART; SM00399; ZnF\_C4; 1.  
 DR PROSITE; PS00031; NUCLEAR\_RECEPTOR; 1.  
 KW DNA-binding; Nuclear protein; Receptor; Transcription regulation;  
 KW Zinc-finger.  
 SQ SEQUENCE 896 AA; 97094 MW; 440F5F6E73BDC796 CRC64;

Query Match 16.9%; Score 748.5; DB 6; Length 896;  
 Best Local Similarity 29.6%; Pred. No. 3,4e-42;  
 Matches 223; Conservative 86; Mismatches 206; Indels 239; Gaps 28;

QY 238 SPNAENGRSHSPAHASNVGSPPLSSPKSSISPSHCSYKSPVSPNNYTLRBSV 297  
 DB 81 SPQVQSRGPGTYLALDEK-----QQPSQOQSAPECHPSGCTPEGGAASAASKGLQOOP 134  
 QY 298 SSPANINNSRCSVSSPNTNRSSTLSSPAATVGSICSPVNAFSTYASGTAGSSTLRD 357  
 DB 135 PAPPDDSDS-----AAPSTLSLGF-----TFPGLSSCGSTDLKD 168  
 QY 358 VVPSPTQKGAQVPPPKTEYESAISNG-VTQGLNIVQYIKPEPDGA---FSSSCLAG 413  
 DB 169 ILSEAGTMQLDQO---QOQOQOQOQFAVSEGNSSGRAR-----EATGAPISSKDSYLG 218  
 QY 414 NSKINSDS-----SFSVPIKQESTKHSCGTSFKGN-----PTVNPV--- 451  
 DB 219 SSTI-SDSAKELCKAVSVSGIGLEHLSPEQLRGDCMTAPLITGPVAPTPCAPL 277  
 QY 452 -----FMDG-----SYFSF----- 460



```

Db 278 AECKSLDLDGPGKSNFEETAEYSPKAGYTKGIDSESLGSSGGEAGSGTLELPALSL 337
QY 461 -----MD-----KDYSLUS-GILGPPV-----478
Db 338 YKSGALDDVAAYPSNDYNNPPLALAGPPPPPHPARIKLENPLDYSAMAAAAAQC 397
QY 479 -GPDGNEGSGFP---VGITQEPDDGSYPEASIPSSAIYG-VNSGGQSHYRIGACTI 533
Db 398 YGDLASLHGGAAPGPGSGSPSATSSSWHTLFTAESQLTGPCCGGGGGNGAAGAVPY 457
QY 534 SLRSARDQSFQH-----LSSFP-PVNTLVES---WKS-----HGD--LS 567
Db 458 GYTRPPGGLAGGGLDALPIDIWPYPGGVSVRPYPSPSCVASEMGPMMWESYSGRPDMRL 517
QY 568 SRNSDGPVLEIYIPENVSSSTLNSVSTGSSRPSTICLVCGDEASGCHYGVYTGSGCVFF 627
Db 518 PTRDHYLPIDYFP-----POKTCLICGDEASGCHYGALTCGCKVFF 560
QY 628 KRAVEGOHNYLCAGRNDCTIDTKRRKNCPCACRLQCLQAGMNGARKSKTKIGKTHPE 687
Db 561 KRAEGKOKTLCASRNDCTIDKFRKNCPCRLKCYEAGHTLGARKLKLGINK-LQEE 619
QY 688 QPQQQOPPPPPPOSPEEGTYYIAPAKEPSVNTALVPOLSTISR---ALTPSPVWLE 743
Db 620 -----GEASSATSPREDA-----QKITVSHIGYEQPIFLVLE 655
QY 744 NIEPEIYAGYDSSKPTAEENLSTLNRLAGKOMIOYVKNKVLPGFKNLPLEDQITLIQ 803
Db 656 AIEGVVACAGHDNNQDPFSALLSLNELGEROLVHYVKNAKALPGFRNLHVDQMAVIO 715
QY 804 YSMWCLSSFALSWSRYKHTNSQFLYFAPDLVENE 837
Db 716 YSMGLVWFAMGMRKSTVNSRMLYFAPDLVENE 749

RESULT 10
042274 PRELIMINARY; PRT; 360 AA.
AC 042274;
DT 01-JAN-1998 (TEMBLrel. 05, Created)
DT 01-JAN-1998 (TEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
DE PROGESTERONE RECEPTOR PROTEIN HOMOLOG (FRAGMENT).
OS Crocodylus siamensis.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Crocodyliidae; Crocodylinae; Crocodylus.
NCBI_Taxid=68455;
RN [1]
RP TISSUE=UTERUS;
RC SWALTANA D., Joerg H., Rieder S., Stranzinger G.;
RT "A crocodile sequence homologous to progesterone receptor.";
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
EMBL: AF030321; AAB81722.1; -.
DR HSSP; P06536; IGDC.
DR InterPro: IPR000536; Hormone_rec_119.
DR InterPro: IPR001723; Sterdhormone_receptor.
DR InterPro: IPR001628; zf-C4.
DR Pfam; PF00104; hormone_rec; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR00398; STRDHORMONER.
DR PRINTS; PR00047; STROIDFINGER.
DR SMART; SM00430; HOLI; 1.
DR SMART; SM00399; znf_C4; 1.
KW DNA-binding; Nuclear protein; Receptor; Transcription regulation;
KW Zinc-finger.
FT NON_TER 1 360
SQ SEQUENCE 360 AA; 40975 MW; 8D5A339AB25905BC CRC64;

```

```

Query Match 16.9%; Score 747; DB 13; Length 360;
Best Local Similarity 58.5%; Pred. No. 1.2e-42;
Matches 141; Conservative 33; Mismatches 49; Indels 18; Gaps 3;

QY 604 LYCGDEASGCHYGVNCGSKVEFFKRAVEGOHNYLCAGRNDCTIDTKIRKNCPCACRLQK 663
Db 1 LIGDEASGCHYGVNCGSKVEFFKRAVEGOHNYLCAGRNDCTIDTKIRKNCPCACRLQK 60
QY 664 LQGMNIGARKSKKLGKLTKEHEBQPOQOPPPPPPPPOSPEEGTYYIAPAKEPSVTAL 723
Db 61. CQAGMVLGGRKFFKFNKVVYRDLVALQSSGLPEBSQALQRLSP-----SPNHDIQF 115
QY 724 VPOLSTISRLTSPVWVLENIPEIYAGYDSSKPTAEENLSTLNRLAGKOMIOYVKN 783
Db 116 VPPV-----ISVLGIEPEYVYAGYDNTKPTPSSLSLNQLEKQLLSVYKN 164
QY 784 AKVLPGRKNLPLEDQITLIQYSWMCSSFALSWSRYKHTNSQFLYFAPDLVFNELLARVR 843
Db 165 SKSLPGFRNLHIDQITLIQYSWMSLWVFLGWRKSYKVGOMLYFAPDLVENE--QRMK 222
QY 844 E 844
Db 223 E 223

```

```

RESULT 11
091AC6 PRELIMINARY; PRT; 359 AA.
ID 091AC6;
AC 091AC6;
DT 01-OCT-2000 (TEMBLrel. 15, Created)
DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
DE MINERALOCORTICOID RECEPTOR (FRAGMENT).
GN MR.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
NCBI_Taxid=8022;
RN [1]
RP TISSUE=TESTIS;
RC MEDLINE=20264048; PubMed=10802282;
RX Colombe L., Postier A., Bury N., Pakdel F., Guiguen Y.;
RT "A mineralocorticoid-like receptor in the rainbow trout, Oncorhynchus
mykiss: Cloning and characterization of the steroid binding domain.";
RL Steroids 65:319-328(2000).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
EMBL: AF209873; AAF61206.1; -.
DR HSSP; P06536; IGDC.
DR InterPro: IPR000536; Hormone_rec_119.
DR InterPro: IPR001723; Sterdhormone_receptor.
DR InterPro: IPR001628; zf-C4.
DR Pfam; PF00104; hormone_rec; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR00398; STRDHORMONER.
DR SMART; SM00430; HOLI; 1.
DR SMART; SM00399; znf_C4; 1.
KW DNA-binding; Nuclear protein; Receptor; Transcription regulation;
KW Zinc-finger.
FT NON_TER 1 359
SQ SEQUENCE 359 AA; 40284 MW; E10983C5109C89A6 CRC64;

```

```

Query Match 16.9%; Score 745.5; DB 13; Length 359;
Best Local Similarity 67.3%; Pred. No. 1.0e-42;
Matches 146; Conservative 24; Mismatches 36; Indels 11; Gaps 3;

QY 627 FKRAVEGOHNYLCAGRNDCTIDTKIRKNCPCACRLQCLQAGMNGARKSKTKIGKTHPE 686
Db 1 FKRAVEGOHNYLCAGRNDCTIDTKIRKNCPCACRLQCLQAGMNGARKSKTKIGKTHPE 60

```

```

QY 687 EQPQQQQPPPPPPPPSPSPSGEGTTIYAPANE---PSVNTALVQ---LSTISRLTLTSPVA 740
Db 61 D-----STPTKRGQGTCPSPGGGVYSSGKEKLESTSPNALVPGPGGLVTPYLPSTICS 115
QY 741 VLENIEPEIIVAGYSSKEDTAENLSTLNRLAGKOMIOVWAKVLPFGKNLPLEDQIT 800
Db 116 VLEIEPEVVFAGYDNTQDPTDHLSTLNQLAGKIMIVWAKVLPFGRLPPIEDQIT 175
QY 801 LIQYSWMLCSFALSWSRYKHTNSQFLYAPADLVFNE 837
Db 176 LIQYSWMLCSFSLSSWSRYKHTNGMLYAPADLVFNE 212

RESULT 12
O9GKN9
ID O9GKN9 PRELIMINARY; PRT; 895 AA.
AC O9GKN9;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ANDROGEN RECEPTOR AR.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_Taxid=9823;
RN [1]
RP
RX MEDLINE=20539123; PubMed=11086548;
RA Trakoujoul N., Ponsuksilli S., Schellander K., Wimmers K.,
RT "A highly polymorphic repetitive polypyrimidine/polyuracine (CCTTT)n
RT sequence in the 5' untranslated sequence of the porcine androgen
RT receptor gene."
RL Anlm. Genet. 31:288-289(2000).
CC -I- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -I- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
DR EMBL; AF161717; AAG40566.1; -.
DR HSSP; P06536; 1GDC.
DR InterPro; IPR001103; Androgen_recep.
DR InterPro; IPR000536; Hormone_rec_1lg.
DR InterPro; IPR001628; zf-C4.
DR Pfam; PF02166; Androgen_recep; 1.
DR Pfam; PF00104; hormone_rec; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR00047; STEROIDFINGER.
DR SMART; SM00430; HOL1; 1.
DR SMART; SM00399; znf_C4; 1.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
KW DNA-binding; Nuclear protein; Receptor; Transcription regulation;
KW Zinc-finger.
SC SEQUENCE 895 AA; 97156 MW; 923C2PDD1F7EA779 CRC64;

```

Query Match	16.8%	Score 741.5	DB 6	Length 895
Best Local Similarity	29.3%	Pred. No. 1e-41		
Matches	222	Conservative	85	Mismatches 204; Indels 247; Gaps 27

  

QY	238	SPNAENRGRSRSPAHASVSGPLSSPLSSMKSSISPPSHCVKSPVSPNNVTLRSV	297
		:	
Db	80	SFOVSRSGTGLALDER-----QPF500GAPCHPESGCTPEPGAASAASKGLQOP	133
QY	298	SSPANINNSRCSVSSPMTNKRSTLSSPAASTVGSICSPVNNAFSTYTAGSSTLRD	357
		:	
Db	134	PAPPEDDSS-----AAPSTLILGP-----TFGLSSCSNDLKD	167
QY	358	VVSPDPTQKGAQVFPKTEVEASISNG-ITGQGLNIVQYIKPPDDG---FSSSCIGG	413
		:	
Db	168	ILSEAGTQMLLOQ---QQQQQQQEAIVSGNSNGAR-----EATGAPISKRSTLYLG	217
QY	414	NSKINSDS-----SFSVPIKQSTKSHCSGTSFKGN-----PIYNPP----	451
		:	
Db	218	SSTI-SDSAKELCKAVASVMGLGVALEHLSPDGLRGCGMYAPLLTGPSPVRRPPCAPL	276

```

QY 452 -----EMD-----SYESP-----460
      ||
Db 277 AEFCKSLDDPGKSNETAETAYSPFKAGYTGGLDSESLGCSGGEGSGTLELPSALSL 336
      ||
QY 461 -----MD-----KDYSSLGILLGPVP-----478
      ||
Db 337 YKSGALDDVAAYPSHDYNYNPLALARPPEPPPHARIKLEPLDYGSAAMAAAAAQC 396
      ||
QY 479 -----GFDNCESGSGFFPGIKQEPDGSYTYPEASIPSAITG-VNSGGQSHYHIGA 529
      ||
Db 397 YGDLASLHGGAAGSGSGSSP-----SATSSSSWHLLFTFAESQILGPCGGGGGGSAGAGA 452
      ||
QY 530 QGTTLSLRSDARDOSEFH-----LSSEFP-PVNTLVYES-----WKS-----HGD 565
      ||
Db 453 VAPYGTHTPPQGLAGQEGDLAI PDIMVPGGVSVHPVPSPSCVKSSEMGPMWESYSGPYGD 512
      ||
QY 566 -----LSSRRBDGYPLEYIPENYSSSTLKSSTGSSRPSKCLVCGDEASGCHGYVYTCGSC 623
      ||
Db 513 MKLEPTRHVLPIIDYFP-----PQKTLICGDASGCHYGALTGSC 555
      ||
QY 624 KYFFKRAVEGQHNHYCAARNDCITDKTRKNCPCACRLOKLOAAMNIGARKSKLGLKG 683
      ||
Db 526 KYFFKRAVEGQHTYCAARNCTITDKPRKNCPCRLKCTCEAGMTILGARKLKLGLK- 614
      ||
QY 684 IHEEDPQOQOPPPPPPPQSPPEEGTITYIAPAKESVNTALVPOLSTSR-----ALTPSPV 739
      ||
Db 615 LOEE-----GEASSATSPTEEPA-----OULTVSHLEGYECOFIL 650
      ||
QY 740 MYLENTIEPIYAGYDSSKPTAENLLSTLRLRAGKOMIQVKKAKVLPGFKNLPLEDOI 799
      ||
Db 651 NYLEAIEGCVACAGHDNNQDPSPFALLSLSLNELGEROLVHYVKKAKLDPGRNLHDDQM 710
      ||
QY 800 TLIQTSWMCLSFALSMRSTYHTNSQPLYPADLVFNE 837
      ||
Db 711 AVIOTSWMGVLVFAFGWRSFTNVNSRLMYTPADLVFNE 748

```

RESULT	13			
P70048		PRELIMINARY;	PRT;	790 AA.
ID	P70048			
AC	P70048;			
DT	01-FEB-1997 (TrEMBLrel. 02, Created)			
DT	01-JAN-1999 (TrEMBLrel. 09, Last sequence update)			
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)			
DE	ANDROGEN RECEPTOR ALPHA ISOFORM.			
GN	XL ALPHA AR.			
OS	Xenopus laevis (African clawed frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae;			
OC	Xenopodinae; Xenopus.			
OX	NCBI_TaxID=8355;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=93376782; PubMed=7690145;			
RA	Fischer L., Catz D., Kelley D.;			
RT	"An androgen receptor mRNA isoform associated with hormone-induced			
RT	cell proliferation.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 90:8254-8258(1993).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=95324753; PubMed=7601302;			
RA	Fischer L.M., Catz D., Kelley D.B.;			
RT	"Androgen-directed development of the Xenopus laevis larynx: control			
RT	of androgen receptor expression and tissue differentiation.";			
RL	Dev. Biol. 170:115-126(1995).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	Kelley D.B., Kamenetz F.R., Kelley D.B., Badea T.C.;			
RL	Submitted (Dec-1998) to the EMBL/GenBank/DBJ databases.			
CC	-I- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).			
CC	-I- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.			
EMBL:	U67129; AAC97386.1; -			
NR	HSSP; P06536; IGDC.			



```

QY 621 GSCVFEKRAVEGONHLYCAGRNDCIIDKIRKNCPCARLOKCLQAGMNLGARKSKLK 680
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 564 GSCVFEKRAVEGOKYLCASRNDCIIDKIRKNCPCARLOKCLQAGMNLGARKSKLK 623
QY 681 LKGIHEBOPQOQPPPPPPSPDEGTYIAPAKESPVTALVPOLSTISR---ALTP 736
    || : || : || : || : || : || : || : || : || : || : || : || : ||
Db 624 LK-LOEGEAS-----TTSPEETT-----OKLTVSHIEGYECOP 658
QY 737 SPVAVLENIEPEIYAGYDSSKPTAENLSTLNRLAGKOMIOYVKKAKYLPFKNLPLE 796
    : || : || : || : || : || : || : || : || : || : || : || : ||
Db 659 IFNLVLAIEGVCACHDNNQDPFALLSLNELGEROLVHVAKKALPGLNLHVD 718
QY 797 DOITLIOYSWMCLSSPALSWSRYKHTNSOFLYFAPDLVENE 837
    || : ||||| || : || : || : || : || : || : || : || : || : ||
Db 719 DOMAVIOYSWMGLMVFPAMGRSFTNVNSRMLYFAPDLVENE 759

RESULT 15
QYGV9 PRELIMINARY; PRT; 848 AA.
ID QYGV9
AC QYGV9;
DT 01-MAY-1999 (Tremblrel, 10, Created)
DT 01-MAY-1999 (Tremblrel, 10, Last sequence update)
DT 01-DEC-2001 (Tremblrel, 19, Last annotation update)
DE ANDROGEN RECEPTOR ALPHA.
OS Anguilla japonica (Japanese eel).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;
OC Anguillidae; Anguilla.
NC NCBL_TaxID=7937;
RN NCBI
RP SEQUENCE FROM N. A.
RC TISSUE=TESTIS;
RX MEDLINE=99119319; PubMed=9918846;
RA Todo T., Ikeuchi T., Kobayashi T., Nagahama Y.;
RT "Fish androgen receptor: cDNA cloning, steroid activation of
RT transcription in transfected mammalian cells, and tissue mRNA
RT levels.";
RL Biochem. Biophys. Res. Commun. 254:378-383(1999).
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
DR EMBL; AB023960; BAA75464.1; -.
DR HSSP; P06536; 1GDC.
DR InterPro; IPR001103; Androgen_recep.
DR InterPro; IPR000536; Hormone_rec_1lg.
DR InterPro; IPR001628; zf-C4.
DR Pfam; PF02166; Androgen_recep; 1.
DR Pfam; PF00104; hormone_rec; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR00047; STROIDFINGER.
DR SMART; SM00430; HOLI; 1.
DR SMART; SM00399; ZNF_C4; 1.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
KW DNA-binding; Nuclear protein; Receptor; Transcription regulation;
KW Zinc-finger.
SQ
SEQUENCE 848 AA; 94692 MW; A8889AF7E2E50D3E CRC64;

```

Query Match 16.4%; Score 727; DB 13; Length 848;  
 Best Local Similarity 31.9%; Freq. No. 8.9e-41;  
 Matches 217; Conservative 87; Mismatches 244; Indels 132; Gaps 27;

```

QY 214 SSTTASFGSPYHSPITOSTPLTCSPTNAENRGRSHSP----AHASNVGSPLSPLSMK 269
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 99 SDAEAPGIFTS-ESSLIDTDEITCKIQSDNOGVRAAGPLLPSSSGCNSGQKSLACTSQ 157
QY 270 SSISPPSHCVSKSPVSPNNYTLRSSVSSPANINNSRCVSSPSN--TNNRSTLSSPAA 327
    : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 158 RETTSGSDTCAGES--CSEHQAT--TISETARELCNAVSYSVLGLNLDLNDNDLSSNOI 212
QY 328 STVGSTICSPVNNAFSTYTAGSTAGSSTL-RDYY-----PSPDIOEKGA-----QEV 372
    : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 213 SSTESDTSQAIYLFESSPGYTGVALVRCDCOSAREGSTSTOYDRGAMFKINRVNDL 272

```

```

QY 373 PPKTEEVEESAIEN-----GYTGQINTVQYIK-PEPDGAFSSSCLGNSKINSDDSFS 424
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 273 PLQPAPEPRHRTSIDAKMDMAGCAQMEHDKSEKCANMDOAHST-----VFSQFDOL 325
QY 425 VPIKQESTKHSCTGSPKKNPTVNPFPMDGSAFSEMDKDYISLSGLGPPVPGDGN 484
    : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 326 LPV---NASHYSONVSVREPOSDFSPL-----YKS-----PGIQKNA 361
QY 485 EGSFGFPGIKOEPPDDGS-----YYPEASIPSSA---IVGVNSGC---QSFH-- 524
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 362 EKINVOYDAITKSEDKGTTSEREMGYOYRINESCSTPSAPPRICAHQNRAGPTNQFFNP 421
QY 525 YRIGAGTISLSRSARDSPQHLSSPPVNTIVE---SWKSHGLDSRRSDGYPLEY-- 579
    : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 422 PEYAKRGVY---SREGYSLEH--GFP--NNLARTPYSGSLAKNELGRLSGPPDVSYRY 473
QY 580 --LPENVSSSLKRSVSTGSSRPSKICLYCGDEASGCHYGVYTGSGCKVFEKRAVEGONH 637
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 474 EGERENVEPVEF-----FFPPORTCLIGDEASGCHYGALTCGSCVFEKRAVEGOKY 527
QY 638 ICAGRNDCIIDKIRKNCPCARLOKCLQAGMNLGARKSKLKLGKGIHEBOPQOQPPPP 697
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 528 LCASINDCTIDKLRKNCPCARLOKCLQAGMNLGARKSKLKLGKGIHEBOPQOQPPPP 575
QY 698 PPPPSPEEGTTYIAPAKESPVTALVPOLSTISRALTSPVAVLENIEPEIYAGYDSS 757
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 576 DGQCGPAEAEALSVSPKYDLGFHTQ-----SMPLN-----ILFAIEPEVYNAGHDYG 622
QY 758 KPDTAENLSTLNRLAGKOMIOYVKKAKYLPFKNLPLEDIOITLIOYSWMCLSSPALS 817
    : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 623 QPDSAAASLTSLNELGEROLVHVAKKALPGLNLHVDQMYIOHSMVAVNVPFALGWR 682
QY 818 SYKHTNSOFLYFAPDLVENE 837
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 683 SFKNVKSRLYFAPDLVENE 702

```

Search completed: September 13, 2002, 10:21:28  
 Job time: 302 sec

*This Page Blank (uspto)*

---

This Page Blank (uspto)